

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 7, 2002, 11:39:21 ; Search time 20.88 Seconds
(without alignments)
2047,881 Million cell updates/sec

Title: US-09-806-088-3

Sequence: 2437
1 MGVGEPGPPRGPAGPAGPL.....DIVRSLSKSGDILWDALYHQ 445

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 71:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1575.5	64.6	444	2	T13155
2	1567.5	64.3	444	2	JG0180
3	448	18.4	449	2	A84900
4	447	18.3	449	2	T50555
5	437	17.9	449	2	T47950
6	414	17.0	458	2	S68358
7	372.5	15.3	447	1	T43119
8	361	14.8	473	1	T26280
9	359	14.7	454	2	H88791
10	335	13.7	523	2	JC7556
11	291.5	12.0	345	2	T36617
12	234	9.6	368	2	S54809
13	210	8.6	359	2	S35157
14	180.5	7.4	370	2	B83034
15	164	6.7	427	2	C70590
16	160	6.6	355	2	D95270
17	155.5	6.4	352	2	B69901
18	155.5	6.4	489	2	H70957
19	152	6.2	359	2	AG2005
20	150.5	6.2	359	2	S52650
21	150.5	6.2	386	2	F95911
22	148.5	6.1	424	2	T07742
23	147.5	6.1	386	2	T02335
24	146.5	6.0	379	2	JC2555
25	145.5	6.0	312	2	S7365
26	145	5.9	377	1	U02337
27	145	5.9	448	2	D85362
28	144.5	5.9	424	2	JC5891
29	144	5.9	383	1	A44227

30	144	5.9	387	2	T07687	omega-6 desaturase
31	142	5.8	443	2	T08136	probable omega-6 d
32	140.5	5.8	351	2	S11519	phosphatidylcholin
33	140.5	5.8	886	2	A59223	nitrate reductase
34	140	5.7	347	2	S43771	phosphatidylcholin
35	140	5.7	380	2	U02338	omega-3 fatty acid
36	140	5.7	380	2	T10898	probable omega-3 f
37	139	5.7	349	2	S43770	phosphatidylcholin
38	138.5	5.7	904	1	R0NTNT	nitrate reductase
39	138	5.7	918	2	A4167	nitrate reductase
40	137.5	5.6	884	2	S66308	nitrate reductase
41	135.5	5.6	287	2	T11959	faty-acid desatur
42	135.5	5.5	414	1	S05441	cytochrome b5-reja
43	135	5.5	447	2	S53309	n-6 fatty acid des
44	134.5	5.5	98	1	U00316	cytochrome b5, ery
45	134.5	5.5	134	1	C8RB5	cytochrome b5, mtc

ALIGNMENTS

RESULT 1

T13155

linoleoyl-CoA desaturase (BC 1.14.99.25) [validated] - human

N.Alternate names: Delta6 fatty acid desaturase; protein DKFZp586C201.1

C.Species: Homo sapiens (man)

C.Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jun-2000

C.Accession: T13155; T08765

R.Cho, H.P.; Nakamura, M.T.; Clarke, S.D.

J. Biol. Chem. 274, 471-477, 1999

A.Title: Cloning, expression, and nutritional regulation of the mammalian Delta-6 des

A.Reference number: Z17612; MID:99085046

A.Accession: T13155

A.Status: Preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-444 <CHO>

A.Cross-references: EMBL:AF126799; MID:94406527; PID:94406528; PIDN:AAD20018.1

R.Mambuti, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, March 1999

A.Reference number: Z16471

A.Accession: T08765

A.Molecule type: mRNA

A.Residues: 138-428, 'D', 430, 'M', 432-444 <WAM>

A.Cross-references: EMBL:AL050118

A.Experimental source: adult uterus; clone DKFZp586C201

C.Genetics:

A.Gene: GDB:FADSD6

A.Cross-references: GDB:9956652

A.Note: DKFZp586C201.1

C.Superfamily: cytochrome b5 core homology

C.Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; unsaturated fa

F:18-94/Domain: cytochrome b5 core homology <CB5>

F:53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 64.6%; Score 1575.5; DB 2; Length 444;

Best Local Similarity 62.6%; Pred. No. 2,1e-124;

Matches 279; Conservative 63; Mismatches 101; Indels 3; Gaps 2;

QY	1	MGVGEPGPPRGPAGPAPLPTFCWDIARADPGKMLYERRKYDISRAQRRPGSR	60
DB	1	MGKGNQG-EGAAERVSVPFSWIEIOKHNLRTRMLVIDRKYYNTKSTSDHPGQR	58
QY	61	LIGHGADATDAFRARFODLNFYRKPLDPLIGELAPESPQSDGPLNAQVEDFRALHQ	120
DB	59	VIGHAGDADATDAFRARFODLNFYRKPLDPLIGELAPESPQSDGPLNAQVEDFRALHQ	118
QY	121	AAEDMKLPDASPTFAFLGHITLAMEVLAWLTYLGPWVSALAAFTLISAQSMCL	180
DB	119	TAEDMKLPKTNHVEFLTLAHTLALSTIAWTFYFGNGWIPLLTATVLAISQAQSMCL	178
QY	181	QHDGHSIFKSWNNHVAQKFTWQGLKFSAHMNNFRFOHAKNPNTFRKDPDTYAPV	240

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Db      179 QHDYCHLSVYRKPKRNHLYKFEVYGHKGSANMWHNRFPQHNKAKPNIFHKDPVNMHLY 238
      241 FLIGE--SSVEYGRKKRRRLPYNOOHLFFELIGPRLTLVNEVENLAWLYCMOMADLLW 299
      239 FVLGEMQPIEGKKRKLKYLPIHNOHEXFFELIGPRLPIRYFOYQIMYIKMNVADLAW 298
Qy      300 AASFYARFELSYLPFGVGLFEFVAVRYLESHEMFVMTQNNHLPKEIGHEKHRDWSS 359
Db      299 ASVYIRFEITYIPFYIGLGLALFLNIRFLESHEMFVMTQNNHLYMELDQADARWESS 358
Qy      360 QLAATCNVPSLFTNMFSGHINQIENHLEPRMRPNRNSRYAPLYKSLCAKHGSLYEYKP 419
Db      359 QLTACNVEQSFNDWFSGHINQIENHLEPRMRPNRNLKIAPLVKSICAKHGLEYOQKP 418
Qy      420 FLTALVDIVRSLLKSGDIDWADYLHQ 445
Db      419 LTRALDIIIRSLKSGKMLMDAYLHK 444

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RESULT 2

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JG0180
Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
C:Accession: JG0180
R:Aki, T.; Shimada, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeta, S.; Ono, K.
Biochem. Biophys. Res. Commun. 255, 575-579, 1999
A:Title: Molecular cloning and functional characterization of rat delta-6 fatty acid des
A:Reference number: JG0180; MUID:99160394
A:Accession: JG0180
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-444 <AKT>
A:Cross-references: DDBJ:AB021980; NID:94514721; PIDN:BA475496.1; PID:94514722
C:Superfamily: cytochrome b5 core homology
C:Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynthe
E:18-94/domain: cytochrome b5 core homology <CB5>
E:53,76/binding site: heme iron (His) (axial ligands) #status predicted

```

```

Query Match          64.3%; Score 1567.5; DB 2; Length 444;
Best Local Similarity 62.8%; Pred. No. 1e-123;
Matches 280; Conservative 63; Mismatches 100; Indels 3; Gaps 2;

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Qy      1 MGVGEPRRSPAPQPGRLPTFCWQIIRAHQDQGDQKLVIRRYVDSIRMAQRHGGSR 60
      1 MCKGNGQ--EGSTELQAPMPFPMETQKNLRTKMLVIDRKYYNVTKSQRRHGGHR 58
Db      61 LIGHGADATDAFAFHQDLNFYKFLQPLLIGELAPESPQDGRPLNAQLVEDRALHQ 120
      59 VIGHSGADATDAFAFHLDLDFVGKFLKLLIGELAPESPQDGRPLNAQLVEDRALHK 118
Qy      121 AEDDKLTDASPTFFAFLIHLIAMEVLALLYLPGWVPSALAAFLIASQASQMSL 180
      119 TAEEDNKLTKHLEFFELLISHIYMESIAFFLIYFGNCHIRPVITAYLATSQAQAWL 178
Db      181 QHDLCHASIFKSWMNVHQAQFYWGOLKGFSAHMMNFRFHQHNKAPNIFHKDPVTAVY 240
      179 QHDYCHLSVYRKPKRNHLYKFEVYGHKGSANMWHNRFPQHNKAKPNIFHKDPDKSLHY 238
Qy      241 FLIGE--SSVEYGRKKRRRLPYNOOHLFFELIGPRLTLVNEVENLAWLYCMOMADLLW 299
      239 FVLGEMQPIEGKKRKLKYLPIHNOHEXFFELIGPRLPIRYFOYQIMYIKMNVADLAW 298
Db      300 AASFYARFELSYLPFGVGLFEFVAVRYLESHEMFVMTQNNHLPKEIGHEKHRDWSS 359
      299 AISTYARFELSYLPFGVGLFEFVAVRYLESHEMFVMTQNNHLYMELDQADARWESS 358
Qy      360 QLAATCNVPSLFTNMFSGHINQIENHLEPRMRPNRNSRYAPLYKSLCAKHGSLYEYKP 419
      359 QLAATCNVEQSFNDWFSGHINQIENHLEPRMRPNRNLKIAPLVKSICAKHGLEYOQKP 418
Qy      420 FLTALVDIVRSLLKSGDIDWADYLHQ 445

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Db      419 LTRALDIIIRSLKSGKMLMDAYLHK 444

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RESULT 3

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A84900
hypothetical protein At2g46210 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: A84900
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vaquer, S.E.; Umayam, L.; Tallon,
eius, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84900; MUID:20083487
A:Accession: A84900
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <STO>
A:Cross-references: GB:AE002093; NID:g3702328; PIDN:AAC62885.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g46210
A:Map position: 2

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Query Match          18.4%; Score 448; DB 2; Length 449;
Best Local Similarity 29.2%; Pred. No. 8.7e-30;
Matches 133; Conservative 63; Mismatches 170; Indels 90; Gaps 17;

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Qy      26 EQIRAHQDQGDQKLVIRRYVDSIRMAQRHGGSRLLIGHGADATDAFAFHQDLNFVR 85
      13 EDLKKNNRPGDLMTISIQGYDVSDWVKSHPGGEAIIIMLAGQDVTDAFIAYHGTAM-- 70
Qy      86 KFLQPLIGELAPESPQDGRPLNAQLVEDRALHQAEDMK--LPD-----AS 131
      71 HLELENGHYVRQHNHSD-----VSRYRL--AAEKRKGLFDKKGHTYTLTLCVG 122
Db      132 PTFEAFLLGHILAMEVLAWL-LYLLPGWVPSALAAFLIASQASQMSCLQNDIGHASIF 190
      123 VMLAAVLITGLVACISIAHDLISAVLLGLMIQSAVYG-----HDSGHYTVT 168
Qy      191 KSMWNHVAQKQFYWGOLKGFSAHMMNFRFHQHNKAPNIFHKDPVTAVFLLGE----- 245
      169 STKPNKLIQLSLGNCILGISTAMKMTNNAHINACNSLDHPDLDHPIPIAVSTKFFNS 228
Qy      246 -SSVEYGRK--KRRYLPNOOHLFFELIGPRLTL--VAFEVE----- 283
      229 MTSRFYGRKLFEDLAFRL--ISYQHTFY---PWCVGRIQLFOTPELLFSKRVYDR 283
Db      284 --NLAYMVCQMOMADLLMAAFYARFELSYLPFGVGLLFF--VAVRYLESHEMFVMTQ 340
      284 ALNTAGLIVFTWTPRL-----VSFLNMQERFIYFVSPAVYALIGHQFC----- 329
Qy      341 MNHLPKEI--GHEKHRDWSSQLAATCNVPSLFTNMFSGHINQIENHLEPRMRPNRNTS 398
      330 LNHFAADVYTPRPNGNMFEKQTAGTLDISCRSFMDWFGGLQFQLEHNLPRILPRCHLR 389
Qy      399 RYAPLYKSLCAKHGSLYEYKPFALTALVDIVRSLLKSG 434
      390 TVSPYVKELCKKHNLPYRSLSMWEANVWITIRLLKNA 425
Db

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RESULT 4

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T50555
delta-8 sphingolipid desaturase [imported] - rape
C:Species: Brassica napus (rape)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Sep-2000
C:Accession: T50555
R:Sperling, P.; Zaehring, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A:Title: A sphingolipid desaturase from higher plants. Identification of a new cytoch
A:Reference number: Z22986; MUID:99003197

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Db      22 KELKHNPNNDWISILGKYVNTTEMAKEHPGDAFLINLAGDVTDAFIAPHFRTAM-- 79
Qy      86 KFLDPLLIGELAPREPSODGPLNAOLVEDPRALHOAEDMKLPDASPFEAFLLGH--IL 143
Db      80 KHLKLTGYNLADYQVSD-----ISRDYRKLAISEFAKAGFEKK-----GHGVLY 125
Qy      144 AMEVLAMLL-----IYLLGPGWPSALAAFIILAIISOASWCLOJDLGHASIFKSMWNH 197
Db      126 SLCEVSLILSACVYGVLYSGSFPI-HMISGALLGLAMQIALTGADACHYQMATRGKMK 184
Qy      198 VAQKFWYQGLKGPSAHMMNFRHQHAKPNIEHKDPDYVAVPELGE-----SSVEYG 251
Db      195 FAGIFGNCITGSIAMWKTNAHHIACNSLDYDPODLHPLMLAVSSKLEFNSTISVFG 244
Qy      252 KK-----KRRYLRYNOOHLFFELIGPRLTLT--VAFEEVNLAVMLVCOMQAD-----LW 299
Db      245 RQLFEDPLAREFVSQ-CHLYLY-----PLMCVARNVLYLQTLILLSRKILPDGLNLIG 298
Qy      300 AASFYARF--FLSTLPEY--GPGVYLFEVNAKVLESHEFWITQMNIIPE--IGHEKH 353
Db      299 TLITWTWEPRLVSRPLPMPERPAVAVISFCVGIQHIQF-----TLNHFSGDYVGPKG 353
Qy      354 RDWVSSQLAATCNVEPSLFTNMFSGHLNFQIEHHLFPRKMRHNSRVAPILVSKCARHGL 413
Db      354 DNWFEPKQGRGTIDACSSWDMFEFGGLQFQLEHHLFPRLRCHLSISPICRELCKKYNL 413
Qy      414 SYEKPPFLTALVDIVRSLK 432
Db      414 PYVSLSFYDANVTTLKTLR 432

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RESULT 7
T43319
Delta5 fatty acid desaturase (EC 1.14.99.~) T13F2.1 [validated] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C:Accession: T43319; T24875
R:Michaelson, L.V.; Napier, J.A.; Lewis, M.; Griffiths, G.; Lazarus, C.M.; Stobart, A.K.
FEBS Lett. 439, 215-218, 1998
A:Title: Functional identification of a fatty acid delta5 desaturase gene from Caenorhabditis elegans
A:Reference number: 222422; MUID:99059458
A:Accession: T43319
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-447 <M1>
A:CROSS-References: EMBL:AF078796; NID:g4003522; PIDD:CA035143.1; PID:g4003523
R:Swindburne, J.
Submitted to the EMBL Data Library, October 1996
A:Reference number: Z19947
A:Accession: T24875
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-197; 'VSHFPNN', 198-447 <M1>
A:CROSS-References: EMBL:Z81122; PIDD:CA03352.1; GSPDB:GN00022; CESP:T13F2.1
A:Experimental source: Clone T13F2
C:Genetics:
A:Gene: CESP:T13F2.1; des-5
A:Map position: 4
A:Introns: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
C:Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

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Query Match      15.3%; Score 372.5; DB 1; Length 447;
Best Local Similarity 24.7%; Pred. No. 1.9e-23;
Matches 113; Conservative 71; Mismatches 173; Indels 101; Gaps 12;

Qy      37 KMLVIERRYDISRMAORHPGSGRLGHHGADATDAFAFODLNFRKFLQGLLGL 96
Db      18 KWCIDDAV-----LRSHGSAITTYKMM-DATTVETFTTGSKKAYQWLT-----EL 65
Qy      97 APESPQ-----DGPL-----MAQVDFRALHOAEDMKLPDAS 131

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Db      66 KKEPTQEPPEIPDKDPRIGIDVVMGTFNISEKRSQINKSFIDLRMVRAEGLMDGS 125
Qy      132 PTFPAFLIGHILAMEVLAMLLIYLLGPGWPSALAAFIILAIISOASWCLOJDLGHASIFK 191
Db      126 PLFYIRKLEITFIILFAFYLOQ--HTYLLPSAI--LMGVAWODLGLTHIEFHHLQFLK 180
Qy      192 KSMNNHVAQKFWQGLKGPSAHMMNFRHQHAKPNIEHKDPDYVAVPELGESSVEYG 251
Db      181 NRYNDLASIFYGVFLQGFSSGCKRKQHVHAAATNVYGRGDDLDVPEY----ATV--- 233
Qy      252 KKKRRLPYNOOHLFFELIGPRLTLVNEVEENLAVMLVCOMADLMAASFARFLSY 311
Db      234 -----AEHLNYSQDSVWMTLFEMQHVHMFEMFRLSLWSLOSLIFVSQMPHY 283
Qy      312 LPFYGVPGV-----LLEFVAVRVLESHEFWITQMNHP 345
Db      284 YDYRRNRAIEQVGLSLHMMWSLQGLFPLDMSTKIMFIVSHLVGGLSHVTVTFHNS 343
Qy      346 KE---IGHEKHDMVSSQLAATCNVEPSLFTNMFSGHLNFQIEHHLFPRKMRHNSRVAP 402
Db      344 VEKPLSSNINMSVACLOMTTRNMRGRFIDMLMGGLNYQIEHHLFPTMRNLTVMR 403
Qy      403 LVKSLCAKHGSLSYEKPPFLTALVDIVRSLKSGDIWLD 440
Db      404 LVKEFAAANGLPYVVDYFTG-----FWLE 428

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RESULT 8
T26280
linoeloyl-CoA desaturase (EC 1.14.99.25) W08D2.4 - Caenorhabditis elegans
N:Alternate names: Delta6 fatty acid desaturase
C:Species: Caenorhabditis elegans
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C:Accession: T26280; T23238
R:Swindburne, J.; Ainscough, R.
Submitted to the EMBL Data Library, March 1996
A:Reference number: Z20188
A:Accession: T26280
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-473 <M1>
A:CROSS-References: EMBL:Z70271; PIDD:CA04233.1; GSPDB:GN00022; CESP:W08D2.4
A:Experimental source: Clone W08D2
R:Napier, J.A.; Hey, S.J.; Lacey, D.J.; Shewry, P.R.
Biochem. J. 330, 611-614, 1998
A:Title: Identification of a Caenorhabditis elegans Delta6-fatty-acid-desaturase by h
A:Reference number: Z21637; MUID:98149727
A:Accession: T37238
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-38, 69-430, 'V', 432-473 <NAP>
A:CROSS-References: EMBL:AF031477; NID:g3088519; PIDD:AA01586.1; PID:g3088520
C:Genetics:
A:Gene: CESP:W08D2.4
A:Map position: 4
A:Introns: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3
C:Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C:Keywords: alternative splicing; oxidoreductase; unsaturated fatty acid biosynthesis

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Query Match      14.8%; Score 361; DB 1; Length 473;
Best Local Similarity 25.3%; Pred. No. 1.8e-22;
Matches 124; Conservative 65; Mismatches 180; Indels 116; Gaps 17;

Qy      37 KMLVIERRYDISRMAORHPGGS-----RLIGHGA----- 67
Db      17 KMLYISEEL-----YKHGPGAVIEQYSIPPLNKNIETRGITTRGSSNALDILYFRN 70
Qy      68 EDAADAFARFQ-----DLNFRK-----FLQPLLIGLAPREPSODGPLNA----- 109
Db      71 SDATHIHFAHSGSSQAYQKQDLKKGHDEFLKQL-----EKRLDKVDIVNSAYDV 124
Qy      110 -----QVDFPRALHOAEDMKLPDASPTFPAFLIGHIILAMEVLAMLLIYLLGPGWPS 163

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Db      25 SVAQEKKNVSEFEKLRKLDHDDLMKANETFLFAKISTLSIMAFATLOL---GXY-- 179
Oy      164 ALAPFILAISOQSWCLOHDLGHSIFKKSMMNHVAKQFVMOGLKGSFAHMMNRHQH 223
Db      180 ITSACLLALMWOQGMWLTJHEFCQDPTKNRPLNDITISLFCGNELOGESRDMKKHNTTH 239
Oy      224 AKRPIFKRDPDYAVPVL-----IGESSVEYKKRRRYLPYNOOHLIFLLIGPPLTLV 278
Db      240 AATFVYIDHDDIDLAPLFAFIPGDLCKYKASPEKAILKIVP--OHLFTMLPML----- 293
Oy      279 NFEVENIAYMYVCMW-----ADLL--MAASFARFELSLYLPFG 316
Db      294 -----RPSMVGOSVOWYFKENMEKYVORNAFWQDQATVGHMAVVFQFLPLPTPLR 347
Oy      317 VPGVLLFVAVRVLESHEFWITQNNH--IPKEIGHK--HRDMVSSQALATCNVPSLFT 373
Db      348 -----VAFITISQMGGLLTAHVTFMHNVSVDKTPANSRLNFFALQILTRNNTPSPFT 403
Oy      374 NWSGHNFOLEHNLPRPRNRYSKVAPLVSLCAKHGLSYEVKPELTALVDIVSLK 433
Db      404 DMLGSLNYOIEHNLFPTRCNLMACKYKEMCKENLPYLVDPDYGYAMNLQOLKN 463
Oy      434 SGD 436
Db      464 MAE 466

RESULT 9
H88791 protein T13P2.1 (imported) - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: H88791
R:Annotation: The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; PMID:99069613; PMID:9851916
A:Note: see webistes genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; 1999; and
A:Accession: H88791
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <STO>
A:Cross-references: GB:chr_IV; PIDN:CA030352.1; PID:q3679828; GSPDB:GN00022; CESP:T13P2.
C:Genetics:
A:Gene: T13P2.1
A:Map position: 4
C:Subfamily: Caenorhabditis elegans Delta6 fatty acid desaturase

```

```

Query Match      14.7%; Score 359; DB 2; Length 454;
Best Local Similarity 24.3%; Pred. No. 2,6e-22;
Matches 113; Conservative 71; Mismatches 173; Indels 108; Gaps 13;

Oy      37 KWLIERRYVDISRWAOHRPGSRLIGHGADATDAFRAFQDINFRKELQBLIGEL 96
Db      18 KWCQIDDAV-----LRSHPGSAITTYKMM-DATVTFHTFTSGSKAYOWMLT-----EL 65
Oy      97 APEBSQ-----DGPL-----NAOLVEDFALQAAEDKKLPDAS 131
Db      66 KKECTQPELPDIKIDPRIGKIDVMMGTFNISEKRSQINKSFIDLMMVRABGIDMGS 125
Oy      132 PTFEFLIGHILAMEVLAMLLILGPGWPSALAFILAIISOQSWCLOHDLGHASIFK 191
Db      126 PLFYIRKLEITFIILFAFYQF--HTYILPSAI---LMSVAMQDGLIHFRPHQDLFK 180
Oy      132 KSMNHVAKQFVMOGLK-----GSAHMMNFRHPOHAKNIFRKRDPDYAVPVLIG 244
Db      131 NRTYIDLASTVCGNFLOYSHIFNNPSSGGKMEQOHAVYHDAITVYVGRGDDLDLPFT-- 237
Oy      245 ESSVEYGGKKRRYLPYNOOHLIFLLIGPPLTLVNFVENIAYMYVCMQAMDLMAASFY 304

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Db      238 -ATV-----ASHLNNTSGDSWMTLPRMCHVHTFMLPFLRLSMILQSLIFV 283
Oy      305 ARFPLSLYPRYGVY-----LFFVAVVLSHNFVW 338
Db      284 SQMPTHYDYITRTAITAYIEOYGLSHMANSLOLYLPDMSTRIMEFLVSHVGGFLSHV 343
Oy      339 TQNNHPRK--IGRKHNDWSSQALATCNVPSLFTNWSGHLNFOLEHNLPRPRH 395
Db      344 VTFNHYSVEKFASSNMSINACLOIMTRNNRPRFRFIDMLGGLNIOIEHNLFPTRH 403
Oy      396 NYSRAVPLVSLCAKHGLSYEVKPELTALVDIVSLKSGDIDW 440
Db      404 NLNTVMPVKEFAANGLPYMWDDYFTG-----FWLE 435

RESULT 10
JC7556 linoeloyl-coa desaturase (EC 1.14.99.25) - Mucor rouxii
N:Alternate names: delta6 desaturase
C:Species: Mucor rouxii
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7556
R:Lacteng, K.; Manontarat, R.; Tanticharoen, M.; Cheevadhanarak, S.
Biochem. Biophys. Res. Commun. 279, 17-22, 2000
A:Title: Delta6-desaturase of Mucor rouxii with high similarity to plant delta6-desat
A:Reference number: JC7556; MUID: 20563795
A:Accession: JC7556
A:Molecule type: DNA
A:Residues: 1-523 <LMO>
A:Cross-references: GB:AF290983
A:Experimental source: strain ATCC 24905
C:Comment: This enzyme, a membrane-bound key enzyme, is responsible for the transform
C:Keywords: oxidoreductase; transformation

```

```

Query Match      13.7%; Score 335; DB 2; Length 523;
Best Local Similarity 24.5%; Pred. No. 3.1e-20;
Matches 120; Conservative 66; Mismatches 193; Indels 110; Gaps 17;

Oy      35 GDKMLVIERRYVDISRWAOHRPGSRLIGHGADATDAFRAFQDINFRKELQBLIG 94
Db      34 GDSVFIEQKYRVNNFMMAKHPGEALRSALGRDVTDEIRTMHP--QVEKELINYCIG 92
Oy      95 ELAPE-----EPSQDGPL-----NAOLVED- 114
Db      93 DYMDDVIRPASMKGQHTFTKPKEDKVLNATWEGGFYQAVDADALQDLKHSHDLKDA 152
Oy      115 -----FRALQAAEDMKLEPDSPTFPFAPFLIGHILAMEVLAMLLITLIG--- 157
Db      153 VLOKDLNGDQIRNAYRKLAELEYAKGLFCN--YKTY-----AREGRTYLLIFLSMF 204
Oy      158 -----PGWPSALAFILAIISOQSWCLOHDLGHASIFKKSMMNHVAKQFVMOGLKGS 212
Db      205 TLKGTETWYHAGAAF--MAFMFQOLVFTADHAGNHEITGKSEIDHVGIVLIANIGLSL 263
Oy      213 HMMNFRFOHNAKPNIFRKRDPDYAVPVLIGESSVE--YGKKRRYLPY-----Q 262
Db      264 GMMKDNINNVHIIYVNHEDPDQIHVFMAITTKFPNNIYSGYRVLYPFAASRFVRRH 323
Oy      324 OHLYFYLL-----LSFGFNLHRLSPAYLLTCKNVTRFLELVGITFFVWVGSLSLPT 379
Oy      315 YG-----VPGVLLFVAVRVLESHEFWITQNNHIFRKHNDWSSQALATCNV 367
Db      360 WNIKAIAYMSYMLTFPLAQITLSHF--CMSTEDRGDDE-----PFRKMLRTMDV 430
Oy      368 EPSLFTNWSGHLNFOLEHNLPRPRNRYSKVAPLVSLCAKHGLSYEVKPELTALVDI 427
Db      431 DCPRMHDMFGGLQYQAVHNLFRPLRNDKCVPLVAKFCDEGLATYKINSGGVV 450
Oy      428 VRSLSKSGD 436

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 7, 2002, 11:36:31 ; Search time 31.33 Seconds
(without alignments)
1577.652 Million cell updates/sec

Title: US-09-806-088-3
Perfect score: 2437
Sequence: 1 MGVGEPGEPGPAQPGAPL.....DIVRLKSGDWMIDAVLHQ 445

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT.*
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17: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT.*
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19: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	% Match	Query Length	DB ID	Description
1	2437	100.0	445	21	AA197540 Human fatty acid d
2	2437	100.0	445	21	AA197540 Human fatty acid d
3	2437	100.0	445	21	AA197540 Human fatty acid d
4	2399.5	98.5	446	22	ABG10280 Novel human diagno
5	2113	86.7	532	22	ABG10280 Novel human diagno
6	1575.5	64.6	444	21	AA197539 Human ORFX ORF1574
7	1575.5	64.6	444	21	AA197539 Human fatty acid d
8	1575.5	64.6	444	22	AA197539 Human fatty acid d
9	1575.5	64.6	444	22	AA197539 Human fatty acid d
10	1575.5	64.6	444	22	AA197539 Human fatty acid d
11	1567.5	64.3	444	22	AA197539 Human fatty acid d

12	1567.5	64.3	444	22	AA197539 Human fatty acid d
13	1565.5	64.2	473	22	AA197539 Human fatty acid d
14	1560.5	64.0	444	21	AA197539 Human fatty acid d
15	1380.5	56.6	432	21	AA197539 Human fatty acid d
16	1380.5	56.6	432	21	AA197539 Human fatty acid d
17	1380.5	56.6	432	21	AA197539 Human fatty acid d
18	1380.5	56.6	432	21	AA197539 Human fatty acid d
19	1380.5	56.6	432	21	AA197539 Human fatty acid d
20	1380.5	56.6	432	21	AA197539 Human fatty acid d
21	1288	52.9	501	22	AA197539 Human fatty acid d
22	1288	52.9	501	22	AA197539 Human fatty acid d
23	1288	52.9	501	22	AA197539 Human fatty acid d
24	1279.5	52.5	444	21	AA197539 Human fatty acid d
25	1279.5	52.5	444	21	AA197539 Human fatty acid d
26	1279.5	52.5	444	21	AA197539 Human fatty acid d
27	1271.5	52.2	444	22	AA197539 Human fatty acid d
28	1271.5	52.2	444	22	AA197539 Human fatty acid d
29	1265.5	51.9	444	22	AA197539 Human fatty acid d
30	1229	50.4	479	22	AA197539 Human fatty acid d
31	1174.5	48.2	322	22	AA197539 Human fatty acid d
32	1174.5	48.2	322	22	AA197539 Human fatty acid d
33	1103.5	45.3	608	19	AA197539 Human fatty acid d
34	1103.5	45.3	608	19	AA197539 Human fatty acid d
35	1103.5	45.3	614	21	AA197539 Human fatty acid d
36	1103.5	45.3	614	21	AA197539 Human fatty acid d
37	1103.5	45.3	615	20	AA197539 Human fatty acid d
38	1077.5	44.2	286	21	AA197539 Human fatty acid d
39	937	38.4	287	21	AA197539 Human fatty acid d
40	934.5	38.3	555	19	AA197539 Human fatty acid d
41	934.5	38.3	555	19	AA197539 Human fatty acid d
42	934.5	38.3	561	21	AA197539 Human fatty acid d
43	934.5	38.3	562	20	AA197539 Human fatty acid d
44	934.5	38.3	562	21	AA197539 Human fatty acid d
45	778.5	31.9	210	22	AA197539 Human fatty acid d

ALIGNMENTS

RESULT 1	AA197540	standard; Protein; 445 AA.
XX	AA197540	
AC	AA197540	
XX	AA197540	
DT	15-JAN-2001	(first entry)
XX	AA197540	
DE	Human fatty acid desaturase 3 protein sequence.	
XX	AA197540	
XX	Human fatty acid desaturase; FADS-1; FADS-2; gene therapy;	
KW	Human; fatty acid desaturase; coronary artery disease; cancer.	
KW	Human; fatty acid desaturase; coronary artery disease; cancer.	
XX	AA197540	
OS	Homo sapiens.	
XX	AA197540	
PN	EP1035207-A1.	
XX	AA197540	
PD	13-SEP-2000.	
XX	AA197540	
PF	09-MAR-1999; 99EP-0104664.	
XX	AA197540	
PR	09-MAR-1999; 99EP-0104664.	
XX	AA197540	
PA	(MULT-) MULTIGENE BIOTECH GMBH.	
XX	AA197540	
PI	Weber BHF, Marquardt A.	
XX	AA197540	
DR	WPI; 2000-559875/52.	
DR	N-PSDB; AAA90954.	
XX	AA197540	
PT	Novel cDNA molecules encoding three human fatty acid desaturases,	
PT	FADS1, FADS2 and FADS3, useful in the treatment of liver disease,	
PT	coronary artery disease and cancer -	
XX	AA197540	

PS Claim 1; Page 44-46; 72pp; English.

CC This sequence is the human fatty acid desaturase, FADS-3, of the
CC invention. An antibody directed against the 3 FADS molecule of the
CC invention (FADS-1, FADS-2, and FADS-3) is useful for diagnostic or
CC therapeutic purposes. The FADS coding sequences are useful in gene
CC therapy. The polypeptide and antibodies are useful in screening for
CC modulating drugs. The polypeptides are also useful for treating liver
CC disease, coronary artery disease and cancer.

CC Note: Two copies of the sequence listing are present within this
CC patent, which contain different sequences. AAA90952 and AAA90955 are
CC both stated as being SEQ ID 1. AAA90956-A90971, and AAA90972-A90987 are
CC stated as being SEQ ID's 7-22.

SQ Sequence 445 AA;

Query Match	100.0%;	Score 2437;	DB 21;	Length 445;
Best Local Similarity	100.0%;	Pred. No. 1.8e-255;		
Matches 445;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MGVGEGRPREDPAPGARPLTFPCMEDIRAHDDPGDKMLVIERRAYDISRNAOHNPGSGR	60
Db	1	mgvgvgrprepdpapgarpltfpcmedirahddpgdkmlvierraydisrnaohnpgsgsr	60
QY	61	LIGHGAEADATDAFRAFHQDINLVYRKFLDPLIGELAREPSPQDRLNALQVDFRALHQ	120
Db	61	l1ghgaeadatdafrafhqdnlvyrkflgpligelarpepsqdrlnalqvdfrralhq	120
QY	121	AAEDMKLPASPTFRFPLIGHLAMEVLAMLYLLGLPGWVSALAAFLAITSQASQML	180
Db	121	aaedmklpasptfrfplighlamevlamlyllglpgwvsalaaflaitsaqswcl	180
QY	181	QHDLGASIFPKKSMWNHYAOKFVNGOLKGFSSAMWNEKRFQHNARPNTEHNDPVTYAPV	240
Db	181	qhdlgasifkkswnhyaoxfvngolkgfssamwnerkfqnarnptehtndpvtvayv	240
QY	241	FLGESSVEYGGKKRRKRYLPYNOQLHFFLGLGPRLLTNMFVEVBNALMYLNCOMARDLMA	300
Db	241	flgessveygkkrkrrylpynoqlhfflglgprlltnmfvevbnalmylncomaradlma	300
QY	301	ASEFAAFSLSYLPFGVPGVLLFFVAARVLESHMFWMIONMHIKREIGHKEHNDWVSQ	360
Db	301	asfyaafslsyrlpfgvpgvllffvaarvleshmfwmiohmhikreighkeghndwvsq	360
QY	361	LAATCNVEBSLEFTNMFSGHLNFQIEHNLPRMPRHNYSRVAPLVKSLCAKGLSLEYKPF	420
Db	361	laatcnvebsleftnmfsghlntfqiehnlpmprrhnysrvaplvkslcahnglsleyevkpf	420
QY	421	LTALYDITVRSIKKSGDINWLDAYLNQ	445
Db	421	ltalvditvrsikksqdlnwldaylnq	445

RESULT	2
AAV83229	
ID	AAV83229 standard; Protein; 445 AA

AC AAY83229;

DT 16-AUG-2000 (first entry)

DE CYB5RP fatty acid desaturase.

KW CYB5RP; fatty acid desaturase; cytochrome b5; macular degeneration;

KW cardiovascular disease; viral infection; virus; identification;

XX

OS Homo sapiens.

FH Key

FT Domain

FT	/label= Cytochrome b5 domain
FT	182..186
FT	/label= His box 1
FT	219..223
FT	/label= His box 2
FT	383..387
FT	/label= His box 3

PN WO200021557-A1

PD 20-APR-2000

PF 05-OCT-1999; 99WO-US23253

PR 09-OCT-1998; 98US-0103760

PA (MERI) MERCK & CO INC.

PI Petrukhin K, Caskey CT;

DR WPI; 2000-317847/27

XX

PT Novel cytochrome b5-related protein useful for identifying modulators
PT useful for treating retinal dysfunction such as macular degeneration,
PT skin diseases, diabetic complications and cardiovascular disorders

PS Claim 3; Figure 3; 44pp; English

CC CYP55RP a fatty acid desaturase and a cytochrome b5-related protein of
CC CYP55RP chemical compositions comprising an activator or an inhibitor of
CC CYP55RP protein are useful for treating macular degeneration. The
CC CYP55RP protein is useful for identifying its activators or inhibitors
CC which are useful for treating abnormal conditions associated with
CC CYP55RP protein activity such as skin disease, diabetic complications,
CC inflammatory and autoimmune disorders, cardiovascular disorders and
CC complications of viral infection. Large amounts of valuable essential
CC fatty acids can be produced by the expression of CYP55RP protein.

SQ Sequence 445 AA;

Query Match	100.0%	Score 2437;	DB 21;	Length 445;
Best Local Similarity	100.0%	Pred. No. 1.8e-255;		
Matches 445; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY	1	MGSGGEGGREGRAORGA	PLRFPCMEQIRAHND	RGKMYLVEBERYUDIS	SRNAORHPGSR	60
Dp	1	mgvggpprpprpaqgag	prlfcwqirahdqgdkv	lvietryddisrwaqnpgrst		60
QY	61	LIGHGAEDATDAFRA	FHODLNVFKELQRL	LIGELAREPSODGR	PLNAQLVEDEFRLHQ	120
Dp	61	lighgaedatdafra	hqdlnfvfkfiprll	ligelapeeqdgrlnaqlvedftrahq		120
QY	121	AAEDMKLPDASPTFFRA	FLNGHILAMEVLANML	LYLLGPGWVSALA	APFLAISQAROSKCL	180
Dp	121	aaedmklfdaasptffa	lllghlamevlawll	lyllgpgwvsalaafllasqagswcl		180
QY	181	QHIDGASITFKRSMMNH	YAOKEFWMGSOIKGFS	SAIMMNRHFOHNAK	PNIFKHDPDTYAPV	240
Dp	181	qhidihasifkkswwnh	aqkftmgqkqfsahwnlfrh	ghakprlnfkhdpdvtvarv		240
QY	241	FLGESSVEYGKKRRRY	LPRYNOOHLVEFFLL	IGRPRLTLVNE	EVENLAUMLUCOMQADLLMA	300
Dp	241	fllgessveygkkrrt	rylpryogrhlyffll	igprlltlvnefevenlaumlvcmqadllwa		300
QY	301	ASTYARFPLSYLRFYGV	GVLLFEVAAVRLSEMF	FWITIQMNHIREKEL	GENEKHKDWTSSQ	360
Dp	301	astyarflsylyrpygv	lllfevavrlsemfwim	lqmhldkpelghkshkhdwssq		360
QY	361	LAATNCVNESTLCNMF	SGNLNPQLEHNLPR	PMRPNHNSRYAR	PLVUSLCAKGLSTSEVPRF	420
Dp	361	laatncvnefstlcnmf	sgnlntqlqlehnlfpr	mpnhnsrvarvlscaaknglseyevkrf		420

OY 421 LPTALVDIVRSLSKSGDIWLDAYLHQ 445
 ||||||||||||||||||
 Db 421 ltaivddivrslsksgdiwldaylhnq 445

RESULT 3

AA025786
 ID AA025786 standard; Protein: 490 AA.

AC AA025786;

XX 16-OCT-2001 (first entry)

DE Human protein sequence SEQ ID NO:1301.

XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW antineoplastic; antineoplastic; antineoplastic; immunosuppressive;
 KW antibacterial; endocrine; cardiac; central nervous system; virucide;
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antineoplastic; anaemia;
 KW antiaggregant; haemostatic; vulnery; antilucer; osteopathic; cytostatic;
 KW dermatological; antiallergic; antiaesthetic; antiparkinsonian; infection;
 KW neuroprotective; antidepressant; neurotropic; antiparkinsonian; infection;
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
 KW antineoplastic; rheumatoid arthritis; septic shock; pancreatitis;
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 KW neurological disorder.

XX Homo sapiens.

XX MO200153455-A2.

XX 26-JUL-2001.

XX 22-DEC-2000; 2000MO-US35017.

XX 23-DEC-1999; 990US-0471275.

XX 21-JAN-2000; 2000US-0487225.

XX 25-APR-2000; 2000US-0552317.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX HPI: 2001-457603/49.

XX N-PSDB; AA099727.

XX Isolated human polynucleotides encoding polypeptides, useful for the

XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -

XX Claim 20; Page 270; 1217Pp; English.

XX AA099166 to AA099904 encode the human proteins given in AA025225 to
 CC AA025963. The proteins can have activities based on the tissues and
 CC cells they are expressed in, such as: antineoplastic; antineoplastic;
 CC antineoplastic; immunosuppressive; antibacterial; endocrine; cardiac;
 CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
 CC cardiovascular; antineoplastic; antiaggregant; haemostatic; vulnery;
 CC antilucer; osteopathic; dermatological; antiallergic; antiaesthetic;
 CC antidiabetic; cytostatic; neuroprotective; antidepressant; neurotropic;
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
 CC encoding them can be used in gene therapy, antisense therapy and vaccine
 CC production. The proteins and polynucleotides are useful for screening for
 CC agonists or antagonists of a protein and for the treatment and diagnosis
 CC of disorders associated with the activity of a protein e.g. inflammation,
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,

CC osteoporosis, severe combined immunodeficiency, eczema, allergic
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
 CC neurological disorders.

XX Sequence 490 AA;

Query Match 100.0%; Score 2437; DB 22; Length 490;
 Best local similarity 100.0%; Pred. No. 2; le-255;
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGVGSEGPREGPAQCAPLPTECFEQTARHPDQKWLTERVYDLSRAORHPGSR 60
 ||||||||||||||||||
 Db 46 mgyvgsepgregpaqgagpplpfecwqtrahpqrqdkxlvterrydstwaqhpqgr 105
 OY 61 LIGHGAEDTDAFRAFHODLNFVKKFLQPLLIGELAPEPSQDGPLNAOLVEDFRALHQ 120
 ||||||||||||||||||
 Db 106 lighgasedtdafrafahodlnfvkflqpllligelaapepsqdpinaqlvedfralhq 165
 OY 121 AAEDMKLFDAAPFEFAFLGHTIAMEVLAMLLITLLGPGWPSALAAFLIAISOQSMCL 180
 ||||||||||||||||||
 Db 166 aaedmklfidaspfflflghlamevawlllyllpgwpsalaafllaiaeqgswcl 225
 OY 181 QHDLGHASIFKSKSMWNVAAQKRYMGOLKGFSAHNNFPHQHHAKPNIFKDPVYVAVP 240
 ||||||||||||||||||
 Db 226 qhdlghasifkkskswnhvaqkitymgqlkgsahwnifhfhghakpnlfhdkpvtvavp 285
 OY 241 FLIGESSVEYGGKKRRRLPYNOOHLFFFLGPPLLTLVNFVENLAVMLVCMQADLLMA 300
 ||||||||||||||||||
 Db 286 fligessveygkkrrrylpyngqhllyfflpplltlvnfeenlavmlvcmqvadllwa 345
 OY 301 ASFYARFFLYLPFGVBPVILLFVAVRYLBSHWVWITOMNHTPKETGHEKHKRDWSSQ 360
 ||||||||||||||||||
 Db 346 asfyarffllylprygvpyllfvaavrylshwvwtomnhpketghekhkrdwvssq 405
 OY 361 LAATCNVEPSLFTNWPSGHLNFOIEHLLPMPRHNTSVAPLVKSLCAKGLSYEVKPF 420
 ||||||||||||||||||
 Db 406 laatcnvepslftnwfsghlnfoiehlmpmrhntsvravlvsckakglisyevkpf 465
 OY 421 LPTALVDIVRSLSKSGDIWLDAYLHQ 445
 ||||||||||||||||||
 Db 466 ltaivddivrslsksgdiwldaylhnq 490

RESULT 4

ABG10281
 ID ABG10281 standard; Protein: 446 AA.

XX ABG10281;

XX 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #10272.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001MO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.
N-PSDB: AAS74468.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

Claim 20; SEQ ID No 40640; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 446 AA;

Query Match 98.5%; Score 2399.5; DB 22; Length 446;
Best Local Similarity 99.1%; Pred. No. 2,1e-251;
Matches 442; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MGVGEGPRGPRGPAOPAPLPFCWEQIRAHNODPGDKMLVIERRYDISRNAQRHGGSR 60
DB 1 mgvgvgepprgpqpaprpftcweqirahndqpgdkwlvierrydisrwagrhpggsr 60
QY 61 LIHGAGADATDARAFHODLNFVRKFLPILIGELAPEPSQDGPPLNAQVDEPRALHQ 120
DB 61 llyghgaedatdarratrhqdntrfkqlpqligelaepsqdgdpplnaqvdepralhq 120
QY 121 AAEEMKLEDSPTFFAFLGHIAMEYLAMLYLLGRCWFSALAAFLAISQASWCL 180
DB 121 aaedmkleidasptffailghilameylawlllyllgprwvpsalaailaisqaswcl 180
QY 181 OHDLGHASIFKRSWMNHNVAOKFVNGOLKFSAHMWNFRFOHNAKPNLEFKDPTVAPV 240
DB 181 qhldghasifkkswmnvnvaokfvmgqlkfsahmwntfrfghakpnllefkdpvtvapr 240
QY 241 FLIGSSSYEYKRRKRLRYNOCHLYRFLIGRPFLTLVFEVBNATMYLVCQWADLMA 300
DB 241 fligsssyeykrrkrylpyngchlyrfligrpfltlvfevbnatmylvcwqadllma 300
QY 301 ASFYARFP-LSYLFYGVGVGLLEFVAVRYSHMFWITOMNHDPKEIGHEKRDWSS 359
DB 301 asfyarfislaylrfygvpgvllffvavrvleeshwftwltgmnhdpkhegkhrdwss 360
QY 360 OLATNCVNEPSELFNMFSGLNFOIEHNLPRMRBNHNSRVAPLKYSICAKHGSLYEKRP 419
DB 361 qlatcnvepselfnmfsglnfoiehnlprmrhnsrvaplvksicakngslsyekrp 420
QY 420 FLTALVDIVSRLSKSGDIMDAYLHQ 445
DB 421 fltalvdivrslsksgdimdaylqh 446

RESULT 5

ABG10280
ID ABG10280 standard; Protein; 532 AA.

XX AC ABG10280;

XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #10271.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001MO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HXSEQ INC.

XX PI Drmanac RT, Liu C, Tang YF;

XX DR WPI: 2001-639362/73.

XX DR N-PSDB: AAS74468.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity

XX Claim 20; SEQ ID No 40639; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 532 AA;

Query Match 86.7%; Score 2113; DB 22; Length 532;
Best Local Similarity 84.0%; Pred. No. 3.5e-220;
Matches 398; Conservative 4; Mismatches 10; Indels 62; Gaps 4;

QY 1 MGVGEGPRGPRGPAOPAPLPFCWEQIRAHNODPGDKMLVIERRYDISRNAQRHGGSR 60
DB 1 mgvgvgepprgpqpaprpftcweqirahndqpgdkwlvierrydisrwagrhpggsr 60
QY 61 LIHGAGADATDARAFHODLNFVRKFLPILIGELAPEPSQDGPPLNAQVDEPRALHQ 120
DB 61 llyghgaedatdarratrhqdntrfkqlpqligelaepsqdgdpplnaqvdepralhq 120

Accession	Protein	Length	Score	E-value
Y121	AAEDKPLPASPSTPEAFLLGIIILAMEVLAWLITLLGPGWVPSALAAFLIAISOASWCL	180	112.1	1.1e-159
Db	121 aeedmkltfaeptcfafllghllamevlewlllyllg	159	112.1	1.1e-159
QY	181 QHDLGASHFFKKSWMNHYAOKFVWGQLKGFSAWMMNFRRFOHNAKRNIFKHKDDPYTAAV	240	111.8	1.1e-159
QY	160 -hdlgashtfkxswmwhvaqfkyngqlkgsfahwmvfrhghakpnlfnhdprcvlaav	218	111.8	1.1e-159
QY	241 FLUGSSVE-----YGRKKRRYLPYNOQH	264	111.8	1.1e-159
Db	219 flilgeesveanlelrltlpgsqdrlarekeevawraavssrtilspqgkkkrrylpyngqh	278	111.8	1.1e-159
QY	265 LKFFLLGPPLLTLVFEVENLAAVYALVCOMADLLMAASFYAAEFLLSYLPFGYGVLLLF	324	111.8	1.1e-159
Db	279 lyfllilgpplltltnvfevenlajmlyvmqgaadllwaasfyarflfslpyfygpyvllff	338	111.8	1.1e-159
QY	325 VAVRVLSEMFVWITQMKHIFKRELGHEKKHDDWVSSQLAATCNVPSLTNNFSGHLAFQI	384	111.8	1.1e-159
Db	339 vaavrvlesmfwywlqgmhlpkelyghknlhdawssqdaatcvepslftnwfsqhlhnlq	398	111.8	1.1e-159
QY	385 EHHLEPRMRHNYSHVADLVYSKCAKHGLSYEVKPFVTAADVIVSLKKSQDIW	438	111.8	1.1e-159
Db	399 eh-----gmprhysrvaplvkslcahnglsyevkpflltalvdvslahnsenf	448	111.8	1.1e-159
RESULT	6			
ID	AA041810			
AA041810	standard; protein; 444 AA.			
AC	AA041810;			
DT	08-FEB-2001 (first entry)			
DE	Human ORFX ORF1574 polypeptide sequence SEQ ID NO:3148.			
KW	Human; open reading frame; ORFX; detection; cytosolic; hepatotropic;			
KW	vulnery; antiporiatic; antiparkinsonian; nootropic; neuroprotective;			
KW	immunovulant; osteoporitic; antiarthritic; immunosuppressant; cardi			
KW	hypotensive; dermatological; immunosuppressive; antihypertoid;			
KW	antiviral; antibacterial; antifungal; antineumatic; antithyroid;			
KW	antianemic; gene therapy; cancer; proliferative disorder; hypertens			
KW	neurodegenerative disorder; osteoarthritis; graft vs host disease;			
KW	cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;			
KW	cholesterol ester storage; systemic lupus erythematosus; infection;			
KW	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;			
KW	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;			
KW	bone damage; cartilage damage; antiinflammatory disease; coagulation;			
KW	thrombosis; contraceptive.			
OS	Homo sapiens.			
PN	MO200058473-A2.			
PD	05-OCT-2000.			
PE	31-MAR-2000; 2000WO-US08621.			
PR	31-MAR-1999; 99US-0127607.			
PR	02-APR-1999; 99US-0127656.			
PR	05-APR-1999; 99US-0127728.			
PR	30-MAR-2000; 2000US-0540763.			
PA	(CURA-) CURAGEN CORP.			
PI	Shinketsu RA, Leach M;			
DR	WPI: 2000-602362/57.			
DR	N-PSDB; AAC76019.			
FT	Useful nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders,			

PT neurodegenerative disorders and cardiovascular disease -

XX Claim 11; Page 2367-2368; 5507pp; English.

CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,

CC which represent the human ORF open reading frames 1 to 3161. The ORF

CC sequences have activities such as: cytostatic; hepatotropic; villartry;

CC antiproliferative; antiparasitism; antitumor; neuroprotective;

CC osteoplastic; anticonvulsant; antihypertensive; immunosuppressive;

CC immunostimulant; cardiac; thrombolytic; coagulant; vasoregulatory;

CC antidiabetic; hypotensive; dermatological; immunosuppressive;

CC antifibrotic; antihypertensive; antiviral; antifungal; antineoplastic;

CC antithrombotic; antineoplastic. The sequences can be used for determining

CC the presence of or predisposition to, or preventing or treating

CC pathological conditions associated with an ORF-associated disorder. The

CC nucleic acids can be used to express ORF proteins in gene therapy

CC vectors. The proteins and nucleic acids may be used to treat cancers,

CC proliferative disorders, neurodegenerative disorders, osteoarthritis,

CC graft vs host disease, cardiovascular disease, diabetes mellitus,

CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus

CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,

CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,

CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,

CC nocturnal haemoglobinuria, anti-inflammatory diseases: to enhance

CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 444 AA.

SO

Query Match 64.6%; Score 1575.5; DB 21; Length 444;

Best Local Similarity 62.6%; Pred. No. 5,8e-162;

Matches 279; Conservative 63; Mismatches 101; Indels 3; Gaps 2;

OY 1 MGGVGERGPRGPAQAGAPLPFFCWEQIRADQDGMVIERVYDYSRMAQRHPGGSR 60

Db 1 mgsgyngng--egaaerevsvpfesweelqkmltdtclwldtkvynlkswelqnpgggr 58

OY 61 LIGHGAEDATDTRAFRFDNLNFVKKTFQRLITIELAPERSODGRLNQLDYEDRALHQ 120

Db 59 vllgysgeatdtdtfdtrfpdtefvkrlfkpllgelapeepsdghknskltdtfdtrlk 118

OY 121 AEDMKLFDAAPTFFAFLIGHTLAMEVLAMLDLILGPGWPSALAAFLTALSQAQSMCL 180

Db 119 taedmlnfknhvffllllahlaiesiaawftvfygngwlrplclafalatsqagawl 178

OY 181 OHLDGASITPKKSKMMWNAQKQFVWGOLGSPFAMMMNRHONHAKNIFGKPDGVAVPV 240

Db 179 ghdgghstvytrkkrwhlthkftvjshlgaasawwmlrhghnakpufikdpdymhlv 238

OY 241 FLIGE--SSVYGGKKKKRRLPYMOCHLITFLIGRPRLILVNEEVENATAMLYCOMQADLM 299

Db 239 fvlgewprleagrkklkyrlpnhqeyfflllgprlllpmfyqvlmtlthvknwadiaw 298

OY 300 AASFVAFPLSLYREYGVGVLFEVAAVAVLSEHMFWMITOMNHIREIGHEKHEDWSS 359

Db 299 avayyliffitylprfyglgallfnlfrfleshwfvwvqgmhlwmedlgeeydwfles 358

OY 360 QLAATCVPESLFTNMGSHLNFQLEHILPRPMRHHYSSRAPIVSLTAKHGLSEVPR 419

Db 359 qlatcvegsffndvfgshlnfglehlfrmptrmlhklaprlvslckngleyekpr 418

OY 420 FLTALVDIVRSLKSGDILWELAYLHQ 445

Db 419 ltrallldlfrslksgklwldaylthk 444

RESULT 7

ID AAY97539

AC AAY97539;

XX 15-JAN-2001 (first entry)

```

XX Human fatty acid desaturase 2 protein sequence.
DE
XX
KW Human; fatty acid desaturase; FADS-1; FADS-2; FADS-3; gene therapy;
KM liver disease; coronary artery disease; cancer.
XX
OS Homo sapiens.
XX
PN EPI035207-A1.
XX
PD 13-SEP-2000.
XX
PF 09-MAR-1999; 99EP-0104664.
XX
PR 09-MAR-1999; 99EP-0104664.
XX
PA (MULT-) MULTIGENE BIOTECH GMBH.
XX
PI Weber BHF, Margardt A;
XX
DR WPI: 2000-558875/52.
XX
DR N-PSDB: AAA90953.
XX
PT Novel cDNA molecules encoding three human fatty acid desaturases,
PT FADS1, FADS2, and FADS3, useful in the treatment of liver disease,
PT coronary artery disease and cancer.
XX
PS Claim 1; Page 41-43; 72pp; English.
XX
CC This sequence is the human fatty acid desaturase, FADS2, of the
CC invention. An antibody directed against the 3 FADS molecule of the
CC invention (FADS-1, FADS-2, and FADS-3) is useful for diagnostic or
CC therapeutic purposes. The FADS coding sequences are useful in gene
CC therapy. The polypeptide and antibodies are useful in screening for
CC modulating drugs. The polypeptides are also useful for treating liver
CC disease, coronary artery disease and cancer.
CC Note: Two copies of the sequence listing are present within this
CC patent, which contain different sequences: AAA90952 and AAA90955 are
CC both stated as being SEQ ID 1. AAA90956-A90971, and AAA90972-A90987 are
CC stated as being SEQ ID's 7-22.
XX
SQ Sequence 444 AA;

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DB 359 qlatcnvegsfnowfsghnlfnqehnlfpmpnhlnklskacghlsgyqk 418
|||
QY 420 FTLALVDIVSLRKSQDITWDAYLRQ 445
|||
DB 419 ltralldltralksksgklwdaylhk 444
|||
RESULT 8
AAE11083
ID AAE11083 standard; Protein; 444 AA.
XX
AC AAE11083;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human delta-6-desaturase (h6d-1).
XX
KW Delta-6-desaturase gene; D6D; lipid metabolism disorder; atopic eczema;
KW mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection;
KW gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome;
KW endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome;
KW cardiovascular disease; Crohn's disease; congenital liver disease;
KW schizophrenia; diabetic neuropathy; nephropathy; retinopathy; cancer;
KW arterial hypertension; atherosclerosis; chronic inflammatory disorder;
KW autoimmune disorder; hypercholesterolemia; atopic disorder; h6d-1;
KW gene therapy; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 53..76
FT /note="Cytochrome b5 motif"
FT Region 180..184
FT /note="His II box"
FT Region 217..221
FT /note="His II box"
FT Region 382..386
FT /note="His III box"
XX
PN WO200170993-A2.
XX
PD 27-SEP-2001.
XX
PF 26-MAR-2001; 2001WO-CA00398.
XX
PR 24-MAR-2000; 2000CA-2301158.
XX
PA (SCOT-) SCOTIA HOLDINGS PLC.
XX
PI Winther MD, Smith HL, Allen SJ, Ponton A, De Antueno RJ;
XX
DR WPI: 2001-611507/70.
XX
DR N-PSDB: AMD19403.
XX
PT Nucleic acid encoding delta-6-desaturase gene useful for treating
PT atopic eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome,
PT gastrointestinal disorders, viral infections and post viral fatigue.
XX
PS Example 4; Fig 6; 164pp; English.
XX
CC The invention relates to polynucleotides that control delta-6
CC desaturase genes (D6D) and methods useful for identifying compounds
CC which inhibit or promote the activity of mammalian D6D. Compounds
CC which modulate D6D gene segments are useful for treating lipid
CC metabolism disorders e.g. atopic eczema, mastalgia, rheumatoid
CC arthritis, Sjogren's syndrome, gastrointestinal disorders, viral
CC infections and post viral fatigue, pre-menstrual syndrome,
CC endometriosis, cystic fibrosis, alcoholism, Alzheimer's syndrome,
CC cardiovascular disease, Crohn's disease, cancer, congenital liver
CC disease, schizophrenia, diabetes and diabetic complications including
CC diabetic neuropathy, nephropathy and retinopathy. Compounds of the
CC invention are also useful for inhibiting progressive and acute

```

CC disorders such as arterial hypertension, atherosclerosis, chronic
CC inflammatory and autoimmune disorders, hypercholesterolaemia and
CC other atopic disorders. Dbd genes are useful in gene therapy. The
CC present sequence is human delta-6-desaturase (hdbd-1).
XX
XX
XX sequence 444 AA.
50

Sequence 444 AA;

Query Match	64.68;	Score 1575.5;	DB 22;	Length 444;
Best Local Similarity	62.68;	Pred. No. 5.8e-162;		
Matches 279; Conservative	63;	Mismatches 101;	Indels 3;	Gaps 2

Qy	1	MGVVGPRGPRRPAQARLPTFCWEDIRADOPGRKMLYIERRYUDISRNAORPGSR	60
Db	1	mgygqgqg--egaaerevsyrlfswedqghmlrtdwlvtdrkynltkwsldhpgqgr	58
Qy	61	LIGHGAEADTATAFARFODLNFYRKVLQPLILGELAREPESODGFLNAOLVEDFRALH	120
Db	59	vishvagedataataitrapdletvylgkllkprlllgelapeespdgknkskldtatlrk	118
Qy	121	AAEDMKLFPASEPFPFARFLGLHLMEMVLAMLLYLLGPGWVSALAAFLTAISQAOSKCL	180
Db	119	taedmmlfktlnhvfllllllahlaieslawfcvfygungvprlrltatyfatsqagwll	178
Qy	181	QHGLGHAISFEKSSMNHNVAOKFVWGGLKGSASIMMNFRRHONNAKPRNFHHKDRDTAVP	240
Db	179	ghnyghlsyytyrckpwnhlyvnhfvgnllkgsaanwnhrhlfqhnakprlnfhnkdrvtmmlhv	238
Qy	241	FLILGG--SSVSEYKKKKRRRLPYNOOHLTFEPLILGPRLLTLVNEEYENLALMYLCSOMADLL	299
Db	239	fvlgewqprleiygkklklyrphnhneyflliprlllrmfyldqvllmnlvlnklnvndlaw	296
Qy	300	AAEFVYARFLSYLPRYGVPGVLLFVVAVRVLDSEHFWETIOMNNHLPKEIGENKKNRWSS	359
Db	299	avsytyrlfctyrlfpyglilgallfnnftrflsehwfwvwtqgmhlymeidgaaydwfss	356
Qy	360	QLAATQNVNPSPLFTWFMFGSHLNFQIENHTEPRRPRNRYSSVAVRYVLSLCAKNGISLTXPR	419
Db	359	qlatcenvqgsffndwefsgnhlnfdlehlfrtmprmlnklaprvkscalcakhgldyegkpr	418
Qy	420	FLPALVDYRSKLKSGDIWDATYALH	445
Db	419	lrrallldlstrlsksgkwldaylnk	444

RESULT	9	
AA093425		
ID	AA093425	standard; Protein: 444 AA.
AC	AA093425;	
DT	06-NOV-2001	(first entry)
DE	Human polypeptide, SEQ ID NO: 3050.	
XX	Human: full length cDNA; cDNA synthesis; oligo-capping.	
XX		
XX		
OS	Homo sapiens.	
XX		
FN	EP130094-A2.	
XX		
PD	05-SEP-2001.	
XX		
PF	07-JUL-2000; 2000EP-0114089.	
XX		
PR	08-JUL-1999; 99UP-0194486.	
PR	11-JAN-2000; 2000UP-0118774.	
PR	02-MAY-2000; 2000UP-0183765.	
XX		
PA	(HELT-) HELIX RES INST.	
XX		
TI	Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawat Y;	
TI	Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H	

XX WPI; 2001-524255/58.
DR N-PSDB; AAK94346.
DR
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation -

PS Claim 8; SEQ ID NO 3050; 1380pp + sequence listing; English

CC The invention relates to primers for synthesising full length cDNA
CC clones, 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'- ends of the cDNA
CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a polypeptide
CC encoded by a full length human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.

Sequence 444 AA;

Query Match	64.68;	Score 1575.5;	DB 22;	Length 444;
Best Local Similarity	62.68;	Pred. No. 5.8e-162;		
Matches 279;	Conservative 63;	Mismatches 101;	Indels 3;	Gaps 2;

Qy	1	MGVGEPSGREGAORGAALPFFCKOIRANDOGDKMLTIERRYVDISRNOHRPGSSR	60
Dd	1	mgyagngy--egadaevsivrflisweeqknhlrltdawldakkyulckwslqnpqqr	58
Qy	61	LIGHGAEDATDAFRAFPHODLNFYAKFLORLULIGELAPEBSODGVLNAOLNEDFRALHQ	120
Dd	59	vighygedatdafraphndiefvgkfklrplljgelapeepsqdbqknskltedfralrk	118
Qy	121	AAEDMKLFDASTPFFAFLLIGHTLMEVLAWLTLTLLGPGWVSALAAFLTASQOMSKL	180
Dd	119	taeemmlfktnhvflllllshlsheslawtvtvyfngvrlpeltatfatsdaqagwl	178
Qy	181	QHDLSHASTFKKSMWNHYAOKFVMQOLKGSFSAHMMNFRIHQHAKRPNTIEKRDPTVAVR	240
Dd	179	qhdygnhsyvrkprkwnhlvkhfvjglnkgaeanwbnhrbqhbkprnlthkdpvnmhlv	238
Qy	241	FLUG--SSVEYGGKKRRYLPYNOCHLVPFLGLPRLTLVNEEYENLTATYLVCOMADLLM	299
Dd	239	fvjgempqleygkklklylphnqhevflljprplljpmvfqyqlmthnlvbkhnvdaw	298
Qy	300	AASTYARFELSTYRPFGEVGVGLFPAVARVLESIMFWIOMNHRIKETGENEKNHDWSS	358
Dd	299	avsyairffltylprfygljgallfnlffirfleshtfwvvcgrmhlymeidgaeyadwss	355
Qy	360	QLAATCNVEBSLETWNVSGHLPFOIENHLFERMRBNHYSVABLVSLCAKHGSLSEYVR	419
Dd	359	qlatcnvegsffndofvsglnhfgiehlfrpmgrnlhkiaplvsklcakngleygekr	418
Qy	420	FLMALDIVRSLKSGDMLTAVLHQ	445
Dd	419	llralldlstrlsksgkwladaaylnk	444

RESULT	10
AAE11084	
ID	AAE11084 standard; Protein; 473 AA.
XX	
XX	AAE11084;
XX	
DT	18-DEC-2001 (first entry)
DE	C-terminal tagged human delta-6-desaturase (h6d-1).
DE	
XX	Delta-6-desaturase gene; D6d; lipid metabolism disorder; atopic eczema;
FW	

KM mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection;
 KM gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome;
 KM endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome;
 KM cardiovascular disease; Crohn's disease; congenital liver disease;
 KM schizophrenia; diabetic neuropathy; nephropathy; retinopathy; cancer;
 KM arterial hypertension; atherosclerosis; chronic inflammatory disorder;
 KM autoimmune disorder; hypercholesterolemia; atopic disorder; hbd-1;
 KM gene therapy; human.

OS Homo sapiens.

XX Key Location/Qualifiers
 XX Region 451..464
 XX FT /note="V5 tag"
 XX FT 468..473
 XX FT /note="6xHis tag"
 XX

PN W0200170993-A2.

PD 27-SEP-2001.

PF 26-MAR-2001; 2001MO-CA00398.

PR 24-MAR-2000; 2000CA-2301158.

PA (SCOT-) SCOTIA HOLDINGS PLC.

PI Winther MD, Smith HL, Allen SJ, Ponton A, De Antueno RJ;

XX WPI: 2001-611507/70.

PT Nucleic acid encoding delta-6-desaturase gene useful for treating
 PT atopic eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome,
 PT gastrointestinal disorders, viral infections and post viral fatigue -
 XX
 PS Example 4; Fig 5; 164pp; English.

CC The invention relates to polynucleotides that control delta-6-
 CC desaturase genes (D6D) and methods useful for identifying compounds
 CC which inhibit or promote the activity of mammalian D6D. Compounds
 CC which modulate D6D gene segments are useful for treating lipid
 CC metabolism disorders e.g. atopic eczema, mastalgia, rheumatoid
 CC arthritis, Sjogren's syndrome, gastrointestinal disorders, viral
 CC infections and post viral fatigue, pre-menstrual syndrome,
 CC endometriosis, cystic fibrosis, alcoholism, Alzheimer's syndrome,
 CC cardiovascular disease, Crohn's disease, cancer, congenital liver
 CC disease, schizophrenia, diabetes and diabetic complications including
 CC diabetic neuropathy, nephropathy and retinopathy. Compounds of the
 CC invention are also useful for inhibiting progressive and acute
 CC disorders such as arterial hypertension, atherosclerosis, chronic
 CC inflammatory and autoimmune disorders, hypercholesterolemia and
 CC other atopic disorders. D6D genes are useful in gene therapy. The
 CC present sequence is C-terminal tagged human delta-6-desaturase
 CC (hbd-1) enzyme.
 CC
 XX
 XX Sequence 473 AA:

SQ

Query Match 64.6%; Score 1575.5; DB 22; Length 473;
 Best Local Similarity 62.6%; Pred. No. 6.4e-162;
 Matches 279; Conservative 63; Mismatches 101; Indels 3; Gaps 2;

QY 1 MCGGCEPRRGRAPLPTFCWQIRAHNDPGRKLVIRRYVDISRAQNRHPSGR 60
 DB 1 mrgkgngq--egaeerevsvptswelqkhlrtidrtwlvldrkynltkwsidqhpqqr 58
 QY 61 LIGHGADATDAFRAFHODLNFRRKFLQPLIGELAPEPSQDPLNAQVDFRALHQ 120
 DB 59 vlyhagadadaftrathpqlfeygfkllpkllygelapepsqdqngksktedfratr 118
 QY 121 AAEDKLPDASPPFFAFLGHILAMEYLAWLILYLGPWVSALAAFLMISQAQSMCL 180
 DB 119 taedmltkthvffllliahlaeslawfcvfyfgngwplclltatvlasqagawl 178

QY 181 QHDGHSITFKSKWNNVAVQKFEVWGOLKGSAAHWNFRHFOHNAKPNTEKDPYTA 240
 DB 179 qhdvghlsyvkprkwnlvbkhvlgthlkgsaanwnhbfghakprnlfbhdpvnm1hv 238
 QY 241 FLAE-SSVEGKKRRRYLPYNOQHLYFFLIGPRLTLVNFVENVLAFMLVCMQADLW 299
 DB 239 fvlgewmpieyggkkllkylpynghyeflljgprlllpmvfygqilmtmvlhknwvdlaw 298
 QY 300 AASFARFELSYLPFGVPGVLLFEVAVRVLDSSHFWITQONHLPKRTGHEKRWVSS 359
 DB 299 avsyariffilylpfygligallflnfrleshwfwvtgmhlvmeidqeaayrdwss 358
 QY 360 QLAATCNVEPSLEFNTPSGHLNFOIEHLEPPRPHNYSRVAPLYKSCAKHGLSYEVK 419
 DB 359 qlatcnvegsffndwfsghlnfgehnlfpmprrnlhklaplvkslcahgyeygekr 418
 QY 420 FLTALVDIVRSLKSGDINWDAYLHQ 445
 DB 419 lltalldivrlsksgklwdaylkh 444

RESULT 11

AA51801

ID AAM51801 standard; Protein; 444 AA.

AC AAM51801;

DT 29-JAN-2002 (first entry)

DE Rat fatty acid desaturase.

DE Rat; fatty acid desaturase; unsaturated long-chain fatty acid production;

KW fermentation.

KW Rattus norvegicus.

OS W0200175069-A1.

PN 11-OCT-2001.

PD 31-MAR-2000; 2000MO-JP02129.

PF 31-MAR-2000; 2000MO-JP02129.

PR 31-MAR-2000; 2000MO-JP02129.

PA (IDEM) IDEMTTSU PETROCHEM CO LTD.

PI Suzuki O, Ono K, Aki T, Shimauchi T, Nakajima T, Kondo A;

XX WPI: 2001-648552/74.

DR N-PSDB; AAI66599.

XX New microorganism for the efficient expression of long-chain

PT unsaturated fatty acids into the medium, comprises Saccharomyces

PT transformed by a fatty acid desaturase gene -

PS Disclosure; Page 26-27; 29pp; Japanese.

XX The present invention relates to a microorganism transformed by a gene

CC encoding a fatty acid desaturase and having the ability to secrete lipids

CC into the medium. This can be used for the efficient production of

CC unsaturated long-chain fatty acids by fermentation. The present sequence

CC is the fatty acid desaturase from Rattus norvegicus.

XX Sequence 444 AA:

Query Match 64.3%; Score 1567.5; DB 22; Length 444;
 Best Local Similarity 62.8%; Pred. No. 4.3e-161;
 Matches 280; Conservative 63; Mismatches 100; Indels 3; Gaps 2;

QY 1 MCGGCEPRRGRAPLPTFCWQIRAHNDPGRKLVIRRYVDISRAQNRHPSGR 60
 DB 119 taedmltkthvffllliahlaeslawfcvfyfgngwplclltatvlasqagawl 178


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XX AAE11082;
AC
XX 18-DEC-2001 (first entry)
DE C-terminal tagged rat delta-6-desaturase (rd6d-1).
XX
XX Delta-6-desaturase gene; D6d; lipid metabolism disorder; atopic eczema;
KW mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection;
KW gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome;
KW endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome;
KW cardiovascular disease; Crohn's disease; congenital liver disease;
KW schizophrenia; diabetic neuropathy; nephropathy; retinopathy; cancer;
KW arterial hypertension; atherosclerosis; chronic inflammatory disorder;
KW autoimmune disorder; hypercholesterolaemia; atopic disorder; rd6d-1;
KW gene therapy; rat.
XX
OS Rattus sp.
XX
XX Key Location/Qualifiers
XX Region 451..464
XX /note="V5 tag"
XX Region 468..473
XX /note="6xHis tag"
XX
XX MO200170993-A2.
XX
XX 27-SEP-2001.
XX
XX 26-MAR-2001; 2001MO-CA00398.
XX
XX 24-MAR-2000; 2000CA-2301158.
XX
XX (SCOT-) SCOTIA HOLDINGS PLC.
XX
XX Winther MD, Smith HL, Allen SJ, Ponton A, De Antueno RJ;
XX WPI: 2001-611507/70.
XX
XX Nucleic acid encoding delta-6-desaturase gene useful for treating
XX atopic eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome,
XX gastrointestinal disorders, viral infections and post viral fatigue -
XX
XX Example 3; Fig 5; 16pp; English.
XX
XX The invention relates to polynucleotides that control delta-6-
XX desaturase genes (D6d) and methods useful for identifying compounds
XX which inhibit or promote the activity of mammalian D6d. Compounds
XX which modulate D6d gene segments are useful for treating lipid
XX metabolism disorders e.g. atopic eczema, mastalgia, rheumatoid
XX arthritis, Sjogren's syndrome, gastrointestinal disorders, viral
XX infections and post viral fatigue, pre-menstrual syndrome,
XX endometriosis, cystic fibrosis, alcoholism, Alzheimer's syndrome,
XX cardiovascular disease, Crohn's disease, cancer, congenital liver
XX disease, schizophrenia, diabetes and diabetic complications including
XX diabetic neuropathy, nephropathy and retinopathy. Compounds of the
XX invention are also useful for inhibiting progressive and acute
XX disorders such as arterial hypertension, atherosclerosis, chronic
XX inflammatory and autoimmune disorders, hypercholesterolaemia and
XX other atopic disorders. D6d genes are useful in gene therapy. The
XX present sequence is C-terminal tagged rat delta-6-desaturase
XX (rd6d-1) enzyme.
XX
XX Sequence 473 AA:
XX

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Query Match 64.2%; Score 1565.5; DB 22; Length 473;
Best Local Similarity 62.8%; Pred. No. 7.8e-161;
Matches 280; Conservative 62; Mismatches 101; Indels 3; Gaps 2;

```

```

QY 1 MGVGEPPRGGPAPGAPLPPTFCWEDIRAHNDQPGKMLVIERKRYVDISRAQARRPGSSR 60
DB 1 mgkgngng--egstslqapmptlrweiqkhnltldrtwlvtdkkyvnlkwsqtrhpg9nr 58

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QY 61 LIGHGAEADATDARAFNODLNFVRKFLDPLILGELAPEPSQDGLNAOLVEDPRAHQ 120
DB 59 vighysgedatdarafrahldldfygfkrlpdligelaapepsldtgyksqtdedfralk 118
QY 121 AAEDMKLPDASPTFPARFLCHIIAMEVLMLLYLIGPFWPSALAEPIAISQASWCL 180
DB 119 laedmnlfkthlhlfflllshllwmeslawfflsyfgngwrlvtlvtalvtalsqagawl 178
QY 181 QHDLCGASIFKFSKSWNNVAQKFVWGCGLKGSFSAHWNFRHFGNHAKRPIFNKDPVFAVP 240
DB 179 qhdylhslvykkskwnlvkfkivghlkgsaanwnhrlfgrhakarplfhhdpdklslhv 238
QY 241 FLGGE-SSEVEGKKRRKRLPYNOOHLFFLIGRPLLTLVNEFEVLEALMYLQMORADLM 299
DB 239 falgewpleygkkklylpynhqhefflfgprlllpmlyfyqdlmnltrtdvdlaw 298
QY 300 AASFYARFFLSYLPFYGVGVLLFEVAVRYLESNMFVITQNNHFKPEIGHKRDWVSS 359
DB 299 alsyyarfflylpylglalvflnflfleshwfvtwltgmnlhymeldldhyrdwfs 358
QY 360 QIATCNVDEPSLFNTMFSGLNFOIEHNLPRKPRHNHNSKVAPLVKSICAKHGLSEYK 419
DB 359 qiaatcnvegslfndwfsghlnfglehhlprmpnhnlkraplvksicakhgleygk 418
QY 420 FTTLVDIVRSLLKSGDINWDAVLIHQ 445
DB 419 ltraldivssllksgevlwdaylhk 444

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RESULT 14
AAV59182
ID AAV59182 standard; Protein; 444 AA.
AC
XX AAV59182;
XX
XX 28-MAR-2000 (first entry)
XX
XX Human oxidoreductase protein (HORP)-5 (clone 008879).
XX
XX Human oxidoreductase protein; HORP; neurological; autoimmune; cancer;
KW reproduction; cell proliferation; vesicle trafficking; endocrine.
XX
XX Homo sapiens.
XX
XX WO200000622-A2.
XX
XX 06-JAN-2000.
XX
XX 29-JUN-1999; 99WO-0514711.
XX
XX 30-JUN-1998; 98US-0091177.
XX
XX 16-JUL-1998; 98US-0155241.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Bandman O, Hillman JL, Tang YT, Lal P, Corley NC, Guegler KJ;
XX Gorysone GA, Baughn MR;
XX WPI: 2000-117171/10.
XX
XX N-PSDB; AA248247.
XX
XX New polypeptide, its antagonist useful for treatment and prevention of
XX neurological, inflammatory, reproductive, endocrine, cell proliferative
XX and smooth muscle disorders
XX
XX Claim 1; Page 80-81; 88pp; English.
XX
XX The invention provides human oxidoreductase proteins (HORP)
XX (AAV59178-183) and nucleic acid sequences (AA248243-248) encoding HORP-1
XX to HORP-6. The HORP proteins can be expressed by standard recombinant
XX methodology. Pharmaceutical compositions comprising the HORP proteins are
XX useful for preventing or treating disorders associated with decreased

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expression or activity of HOPR while HOPR antagonists are useful for preventing or treating disorders associated with increased expression of HOPR. Such disorders include neurological, autoimmune, reproductive, cell proliferative, vesicle trafficking, endocrine disorders and cancer in mammal, especially in humans. HOPR is useful for producing antibodies and for drug screening using libraries of compounds. HOPR polynucleotides and their antibodies are useful for diagnosis of disorders associated with HOPR expression. The present sequence represents the HOPR-5 Protein.

Sequence 444 AA:

Query Match 64.0%; Score 1560.5; DB 21; Length 444;
 Best Local Similarity 62.3%; Pred. No. 2.5e-160;
 Matches 278; Conservative 62; Mismatches 103; Indels 3; Gaps 2;

1 MGVGEPGREGPAOCALPFCWEOIRAHODPGDKWIVERRVYDISRMAQRHFGSR 60
 1 mfgkgnqg-egaaerevavptswelqkhnltstsglvldtkyulktkwsqnp99qr 58
 61 LIGHGAEDATDAFRAFHODLNFVRKFLQPLIGELAPEPSQDGPLNQLVEDFRALHQ 120
 59 vishyagedatdfrfhpolefvgfkfpllgelapepsqdhgknkctedfralrk 118
 121 AABDMKIFDASPTFEAPLGHILAMVLAAMLIIYLGPQWPSALAAFLIAISQAOSKCL 180
 119 taedmlfthvffillliahllaleslawfvtvfyggnwiprlitafvlatseqaqayl 178
 181 QHDLGNASTFKKSMNHNVAOKFVMGOLKGFSAHMMNFRHONHAKNPHEKDPDVAVPY 240
 179 qhdyghlsvytrkpkwhlvhkytghlkgasawwhrhqhnakpnlthkdpdmllhv 238
 241 FLTGE-SSVYGGKRRRYLPYNOOHLFFLIGPRLTLVFEVENLAYMLQCMADLLM 299
 239 fvgewqpiygykklkyrpyrhqheffligrpllpmfyqqlmtahvknwldaw 298
 300 AASFYARFLSYLPFYGVPGVLLFVAARVLESHEFWITQNMHLPKEIGHEKHWDVSS 359
 299 avsytrffitylrfyglgallfllfrfleshwfvtvqgmhlvmeldgeayrdwfs 358
 360 QLATCWESLFTNMFSGHNFQIEHHLPKRPKNHYSVAPLVSLCAKHLSTYVKKP 419
 359 qlatcnvegsfndwfsghnftqlehlfrmpmrlhkiaplvsloakngleyqekp 418
 420 FLTALVDIVSLKSGDIWDAVLIHQ 445
 419 ltralliditrsiksgklwdaylkh 444

RESULT 15
 AAY95446
 ID AAY95446 standard; Protein; 432 AA.
 XX AAY95446;
 AC AAY95446;
 XX 10-OCT-2000 (first entry)
 XX Human delta-5-desaturase-related contig 253538a-encoded protein.
 DE Delta-5-desaturase; human; polyunsaturated fatty acid;
 KW arachidonic acid; eicosapentaenoic acid; docosapentaenoic acid;
 KM docosahexaenoic acid; nutrition; feedstuff.
 XX Homo sapiens.
 OS Homo sapiens.
 XX 00200040705-A2.
 PN 03-JUL-2000.
 XX 29-DEC-1999; 99MO-US31163.
 XX 08-JAN-1999; 99US-0227613.
 PR

XX (ABBO) ABBOTT LAB.
 PA Mukerji P, Leonard AEX, Huang Y, Parker-Barnes JM,
 XX WPI: 2000-465975/40.
 DR N-PSDB: AAA4939.
 XX New polypeptide useful for preparation of nutritional supplements based
 PT upon human DELTA5-desaturase, desaturates polyunsaturated fatty acids
 PI at carbon 5 -
 XX
 PS Example 1: Fig 9; 127pp; English.

XX The present sequence is that of the polypeptide encoded by the
 CC partial open reading frame of contig 253538a (see AAA4939). The
 CC translated sequence shows homology to Mortierella alpina
 CC delta-5-desaturase and delta-6-desaturase sequences, suggesting a
 CC human desaturase-like protein. The contig was utilised in the
 CC isolation of cDNA (see AAA4932) encoding human delta-5-desaturase
 CC (see AAY95445). Delta-5-desaturase catalyzes the conversion of
 CC dihomogamma-linolenic acid to arachidonic acid and of 20:4n-3 to
 CC eicosapentaenoic acid. Recombinant enzyme, expressed in prokaryotic
 CC or eukaryotic hosts using the isolated human delta-5-desaturase
 CC cDNA, can be used in the production of polyunsaturated fatty acids
 CC that may be added to nutritional, veterinary and pharmaceutical
 CC compositions.
 CC
 CC Sequence 432 AA:

Query Match 56.6%; Score 1380.5; DB 21; Length 432;
 Best Local Similarity 57.7%; Pred. No. 8.2e-141;
 Matches 248; Conservative 66; Mismatches 113; Indels 3; Gaps 3;

19 PPT-FCWEOIRAHODPGDKWIVERRVYDISRMAQRHFGSGRLIGHGAEDATDAFRA 77
 3 ppyrfvtdewvqrgsgeerwlvldtkyuliseftirpbgsvrvshyagdadcpvaf 62
 78 HODLNFVRKFLQPLIGELAPEPSQDGPLNQLVEDFRALHQAEDMKLPDASPTFEAF 137
 63 hlnkgvkkymsslllgelspeqsfepknlctedfrelratvernglmkanhvfl 122
 138 LGHILAMVLAAMLIIYLGPQWPSALAAFLI-MISQAOSKLOHDLGNASTFKKSMN 196
 123 yllhllldgaawltlwtgtsflprllcaavllsavqgaqawldyghlsvytrkpkwn 182
 197 HVAOKFVMGOLKGFSAHMMNFRHONHAKNPHEKDPDVAVPYVLGE-SSVEYGGKRR 255
 183 hlvhkfvtvghlkgasawwhrhqhnakpnlthkdpdmllhvfgewqpiygykkl 242
 256 RYLPYNOOHLFFLIGPRLTLVFEVENLAYMLQCMADLLMAASFYARFLSYLPFY 315
 243 kypvryrhqheffligrpllpmfyqqlmtahvknwldawvayytrffitylrfy 302
 316 GYPCVLLFVAARVLESHEFWITQNMHLPKEIGHEKHWDVSSOLAATCNVPSLFTNM 375
 303 gligallfllfrfleshnftvwtqgmhlvmeldgeayrdwfsqtlatcnvegsfndw 362
 376 FSGHNFQIEHHLPKRPKNHYSVAPLVSLCAKHLSTYVKKPFLTALVDIVSLKSG 435
 363 fsghlnftqlehlfrmpmrlhkiaplvsloakngleyqekprralliditrsiksg 422
 436 DIWDAVLIHQ 445
 423 klwdaylkh 432

Search completed: October 7, 2002, 11:40:50
 Job time: 259 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 7, 2002, 11:41:16 ; Search time 13.41 Seconds

(Without alignments)
1284,877 Million cell updates/sec

Title: US-09-806-088-3

Sequence: 1 MGSEVGPREGPAGAPL.....DIVRSIKSGDIDWLVYHQ 445

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40:*

Print No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Match	Length	DB	ID	Description
1	210	8.6	359	1	LICD_SYNY3	008871 synechocyst
2	148.5	6.1	424	1	PD6C_SOYBN	P48628 glycine max
3	147.5	6.1	386	1	PD3E_ARATH	P48623 arabidopsis
4	146.5	6.0	379	1	PD3E_TORAC	P48626 nicotiana t
5	145	5.9	377	1	PD31_BRANA	P46311 brassica na
6	145	5.9	448	1	PD6C_ARATH	P46312 arabidopsis
7	144	5.9	383	1	PD31_BRANA	P48624 brassica na
8	144	5.9	387	1	PD61_SOYBN	P48620 glycine max
9	142	5.8	443	1	PD6C_BRANA	P48627 brassica na
10	141	5.8	383	1	PD6E_ARATH	P46313 arabidopsis
11	140.5	5.8	351	1	DSGA_SYNY3	P20388 synechocyst
12	140.5	5.8	886	1	NR1I_SOYBN	P54233 glycine max
13	140	5.7	380	1	PD3E_PHAUV	P32231 phaseolus a
14	140	5.7	380	1	PD3E_SOYBN	P48625 glycine max
15	138.5	5.7	904	1	NR1I_TORAC	P17569 nicotiana t
16	138	5.7	918	1	NR1A_CUCMA	P17569 cucurbita m
17	137.5	5.6	890	1	NR1A2_SOYBN	P39870 glycine max
18	135	5.5	384	1	PD6E_ARATH	P39867 brassica na
19	135	5.5	414	1	PD6C_ARATH	P48629 spiraea ol
20	135	5.5	447	1	PD6C_SPILO	P48629 spiraea ol
21	134.5	5.5	133	1	PD3E_ARATH	P00169 arctostaphy
22	133	5.5	460	1	PD3C_RITCO	P48619 ricinus com
23	132	5.4	133	1	CYB5_BOVIN	P00171 bos taurus
24	132	5.4	904	1	NR1A2_TORAC	P08509 nicotiana t
25	130.5	5.4	133	1	CYB5_HORSE	P00170 sus scrofa
26	130.5	5.4	133	1	CYB5_PIG	P17570 lycopersico
27	130.5	5.4	911	1	NR1A2_SOYBN	P48620 glycine max
28	130	5.3	447	1	PD3C_SESTN	P00175 saccharomy
29	129.5	5.3	591	1	CYB2_YEAST	P39866 phaseolus v
30	129.5	5.3	890	1	NR1A2_PHAUV	P00174 gallus gall
31	129	5.3	138	1	CYB5_CHICK	G04794 spirulina p
32	129	5.3	351	1	DSGA_SPILO	P39869 lotus japon
33	129	5.3	900	1	NR1A2_TORAC	

34	128.5	5.3	920	1	NR1A_CICIN	P43101 cichorium i
35	128	5.3	133	1	CYB5_HUMAN	P00167 homo sapien
36	128	5.3	135	1	CYB5_CUSRE	P49097 susculca ref
37	127.5	5.2	120	1	CYB5_YEAST	P40312 saccharomy
38	127	5.2	881	1	NR1I_PHAUV	P39865 phaseolus v
39	127	5.2	911	1	NR1I_BRANA	P39867 brassica na
40	126.5	5.2	87	1	CYB5_ALOSE	P00168 alouatta se
41	126.5	5.2	917	1	NR1I_ARATH	P19322 arabidopsis
42	126	5.2	911	1	NR1A2_BRANA	P39868 brassica na
43	125	5.1	453	1	PD3C_SOYBN	P48621 glycine max
44	125	5.1	573	1	CYB2_HANAN	P09437 hansensula a
45	124.5	5.1	133	1	CYB5_MOUSE	P56395 mus musculu

ALIGNMENTS

```
RESULT 1
ID LICD_SYNY3 STANDARD; PRT; 359 AA.
AC 008871;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Linoeoyl-CoA desaturase (EC 1.14.99.25) (Delta(6)-desaturase).
GN DSE6 OR SLU0262.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
ON NCBI_Taxid=1148;
RX MEDLINE=93283633; PubMed=8389613;
RA Reddy A.S., Nuccio M.L., Gross L.M., Thomas T.L.;
RT Isolation of a delta 6-desaturase gene from the cyanobacterium
RT Synechocystis sp. strain PCC 6803 by gain-of-function expression in
RT Arabidopsis sp. strain PCC 7120.
RL Plant Mol. Biol. 22:293-300(1993).
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Keneke T., Sato S., Kotani H., Tanaka A., Asanizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugliura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Katuo K.,
RA Okumura S., Shimp S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT *Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
-1- CATALYTIC ACTIVITY: Linoeoyl-CoA + AH(2) + O(2) = gamma-
Linoeoyl-CoA + A + 2 H(2)O.
-1- COFACTOR: IRON.
-----
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-----
DR EMBL; L11421; AAA27286.1; -
DR EMBL; D90914; BAA18502.1; -
KW Oxidoreductase; Iron; Complete proteome.
SEQUENCE 359 AA; 41425 MW; 33PB165AEB98C05F CMC64;
```

Query Match 8.6%; Score 210; DB 1; Length 359;

Best Local Similarity 24.7%; Pred No. 6.4e-10; Mismatches 125; Indels 94; Gaps 17;

Matches 85; Conservative 40; Mismatches 125; Indels 94; Gaps 17;

149 AMLIYLIGPEWWD-SALAAFIATISQAO-SWCLOHDLGHASIFKSMNHHV---AQREV 203

```

Db 54 AWAFF-LEPAVIFPVLLGCKVLAIALAAFSFNVGHDANMNASSNPINRYLGMTYDFV 112
QY 204 MGQLGSEFAMMMRRH--FOHAKNPENHKDDYVAAPVLLGSSSEYKRRRLPNO 262
Db 113 -----GLSSFLMKRYRHHNTYTNILGNDVEIH-----GGGAVRMSPEDEHYGYTF 160
QY 263 QH-----LYFFLIG-----PRLTLVNFVEVENIAYLVCMQAD 296
Db 161 QQFYIMGLYLFIPFYWFYLDVYLVANKGKYHDKHIPP-----FQPLEIASIL-----G1K 210
QY 297 LIMAASFARFELSLP-----YGVGYLL-----FPVANRYLVESHMFYVI 338
Db 211 LMLGYVG-----LPLALGFSIPEYLVIGASTYTYMTGYCTIPMLAHVLESTEL-- 262
QY 339 TQMHNPKEIGHKRDVSSQLATCN--VEPSLFTNMFSGHLNQIEHRLPRMRHNY 397
Db 263 -----TPGSEGAIDDEALICQITNTANFNPNFNNWCGGGINHQVYTHLPRNICHY 317
QY 398 SRAVPLVRSKCAKHGLSEYKPFELALVDIVRSKSKSGDWLDA 441
Db 318 PLENIITDVCQEGVEKYPTFKAI-----ASNTRWLEA 354

RESULT 2
FD6C_SQYBN STANDARD; PRT; 424 AA.
AC P48628:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.99.-).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=94345008; Pubmed=8066133;
RA Hitz W.D., Carlson T.J., Booth J.R. Jr., Kinney A.J., Stecca K.L.,
RA Yadav N.S.;
RT "Cloning of a higher-plant plastid omega-6 fatty acid desaturase cDNA
RT and its expression in a cyanobacterium.";
RL Plant Physiol. 105:635-641(1994).
CC -1- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC or send an email to license@isb.slb.ch).
CC -----
CC EMBL: L29215; AAA50158.1; -
CC InterPro: IPR001225; FA_desaturase.
CC Pfam: PF00487; FA_desaturase; 1.
CC ProDom: PD001081; FA_desaturase; 1.
CC Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
CC Transf. peptidase.
CC TRANSIT 1 63 CHLOROPLAST (BY SIMILARITY).
CC CHAIN 64 424 OMEGA-6 FATTY ACID DESATURASE.
CC DOMAIN 165 169 HISTIDINE BOX 1.

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FT DOMAIN 201 205 HISTIDINE BOX 2.
FT DOMAIN 361 365 HISTIDINE BOX 3.
SQ SEQUENCE 424 AA; 49641 MW; 4F3DE52D4B1A2009 CRC64;

Query Match 6.18; Score 148.5; DB 1; Length 424;
Best Local Similarity 19.9%; Pred. No. 8.1e-05;
Matches 74; Conservative 62; Mismatches 146; Indels 89; Caps 17;

QY 75 RAFHODLVFRKFLQPLLIGELAPEPS--QDGLNALQVED--PRALHO--AEDMKLFD 129
Db 44 KFRQRNRFTVRKNVTVYIHAVALPQDAPAPESAEYKQLAEDYGRQVGEPLSDVTLKD 103
QY 130 A-----SPTEFAFLGHILAMEV-----LMLLTYLLGPGW 161
Db 104 VINPLRKEVEFIDDKAMKSYLISVTSYA--LGLFMISKAPWYLLPLAMV-----WT 153
QY 162 PSALAFLITAIQAQNSMCLOHDGHASIFKSKMNVHVAQKFPWGOLKQGSAMH-----WNF 217
Db 154 GYATIGFV-----IGHDCAH-----RSPSSKLVEDIVGLLAWPLIYPERRRF 199
QY 218 RHOHNAKPNIEHKDPDYVAAPVFL-----LGESSVEYGRKKRRYLPYN--QQHLYFF 268
Db 200 KDRHRHAKTNMLRE--DTAMHPWAKDEFESTPLRKALTYG-----YGFRCMNSIAHWL 252
QY 269 ILGRLPLFLVNFVEVENIAYLVCM--QWADLMAASFARFELSYLPFYGVGVLLFQVAV 327
Db 253 MNHFLKFRSEVPRKISLACVFALIGWPLIIYKKGIMGWIKFLMWLGTHF--- 309
QY 328 RYLSHMFVWITQNNHNPKEIGHKRDW--VSSQLATCNVEPSLFTNMFSGHLNQIE 385
Db 310 -----NMSTFTVWVHAPYIIPKYSSEWNRQAQNLGTGHDYRKWIELIICHQINVIP 363
QY 386 HHLFPRMPRHN 396
Db 364 HHISPRIPSYN 374

RESULT 3
FD3E_ARATH STANDARD; PRT; 386 AA.
AC P48623:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.99.-).
GN PAD3 OR AT2G29960 OR F23F1.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA; TISSUE=Seedling;
RX MEDLINE=94302147; Pubmed=8029334;
RA Yadav N.S., Wierzbicki A., Aegerter M., Caster C.S., Perez-Grau L.,
RA Kinney A.J., Hitz W.D., Booth J.R. Jr., Schneider B., Stecca K.L.,
RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
RA Fiedmann K.A., Pierce J., Browe J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases.";
RL Plant Physiol. 103:467-476(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA; TISSUE=Hypocotyl;
RA Watahiki M.C., Yamamoto K.T.;
RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RX MEDLINE=94345020; Pubmed=8066143;
RA Nishitani T., Nishimura M., Aronow V., Iba K.;
RT "Genomic nucleotide sequence of a gene encoding a microsomal omega-3

```

fatty acid desaturase from Arabidopsis thaliana; plant physiol. 105:767-768(1994).

[M]

SEQUENCE FROM N.A.
RC SHRRAIN-CV. COLUMBIA;
RX MEDLINE-20083487; PubMed=10617197;
Rlin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Blum J.J.C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldguy L.V.,
Snell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Ko H.T.,
McFitt A.S., Cronin L.A., Shen M., Pai G., Van Aken S., Unayam L.,
Ra Hoffman E.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
A Goodman W.C., Somerville C.R., Cohenavner G.P., Preiss D.,
Nierman H.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana";
RT Nature 402:761-768(1999).
CC - FUNCTION: MICROSOMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOlipids.
CC - PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC - SUBCELLULAR LOCATION: Endoplasmic reticulum.
CC - TISSUE SPECIFICITY: ABUNDANT IN LEAVES AND SEEDLINGS. BARLEY
CC DETECTABLE IN ROOT TISSUE.
CC - DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC - SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

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DR EMBL; L22931; AAA61778.1; --
DR EMBL; D17579; BAA05450.1; --
DR EMBL; D26508; BAA05514.1; --
DR EMBL; AAC004680; AAC31854.1; --
DR InterPro: IPRO01225; FA.desaturase.
DR Pfam: PF00487; FA.desaturase; 1.
DR ProDom: PD001081; FA.desaturase; 1.
KM Oxidoreductase; fatty acid biosynthesis; Endoplasmic reticulum;
KN Transmembrane.
KT TRANSMEM 63 POTENTIAL.
FT TRANSMEM 220 POTENTIAL.
FT TRANSMEM 242 POTENTIAL.
FP DOMAIN 101 HISTIDINE BOX 1.
FP DOMAIN 137 HISTIDINE BOX 2.
FP DOMAIN 304 HISTIDINE BOX 3.
SQ SEQUENCE 386 AA; 4407 MW; 6AEAEA2692BB5516 CRC64;

Query Match 6.1%; Score 147.5; DB 1; Length 386;
Best Local Similarity 21.8%; Pred. No. 8.Be-05;
Matches 80; Conservative 40; Mismatches 110; Indels 137; Gaps 21.

Dy 160 WVPS-----ALAFLAIISQAQS-----CLOHDDGSHAS 188
Dy ||||| :||||:
Db 48 WKSPRLSMSESYVRDIIVVAIALAAVVVDVSFWLPPLTWMAAGTLFMALVLGHDSHGHS 107
Qy 189 I-----FKKSWNNNAOKFYWGDLKGSSAHMMWFREFFHNHK-----PRHP 230
Qy FSDFIRLLANSYGVIHLSTFI-----VPRIWGRNISIRTIHQNHGNHVNDSDSVLRPEAYX 162
Db 108 FSDIFRLANYSVGIIHTSLFI-----VPRIWGRNISIRTIHQNHGNHVNDSDSVLRPEAYX 162
Qy 231 KDPPVT-----VAEPVFLAGESSVEYGGKKRRRYLDYNOOHLYPFLIGRPILLTY 278
Dy ||||| :||||:
Db 163 KLIPSTMLRVTVLPDALAPLVLYLCYRSR-----GKEGSHFNFNS-----LEAFS----- 208

OY 279 NFEENJLAKYKLOMADLLMAASFARRETSJ-----LPEFGVGVLLFVAVRVLE 331
 Db 209 --ERKLIATSTG-----WSIMEVSLTALSFVGPVLAKYGVGYIT--FVM----- 252
 OY 332 SHWVWITONNHIPKEIGEHKRDWVSSOL-----AATCNVPSLFTWMPGSHNFOI 384
 Db 253 --WIDANTYLIHH-----HGHDEKLPYWRCKGEMSYLNGSLTTIDRDYIGFNN--IHMDIGTAV 305
 OY 385 EHHFPPMPHPNHSRVAAPLYKSI--CAKHLS--YKXPEPLTALYDI-----VPSLKK--- 433
 Db 306 IHHLEPDIPIRYH-----LYDATKAAKHYGLGTYNEPXTSGALITHLYVESLVASIKDHY 359
 OY 434 ---SGDI 437
 Db 360 VSDIGDI 366
 RESULT 4
 FD3E_TOBAC STANDARD: PRT; 379 AA.
 AC FD3E_TOBAC P48626;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, last sequence update)
 DT 01-MAR-2002 (Rel. 41, last annotation update)
 DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.99.-).
 GN PAD3
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asperidiales; eusterserids I; Solanales; Solanaceae; Nicotiana.
 ON NCBI_TextID=4097;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, SRL; TISSUE=leaf;
 RA MEDLINE=95011632; PubMed=7926817;
 RA Hamada T., Kodama H., Nishimura M., Iba K.;
 RT "Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase.";
 RL Gene 147:293-294(1994).
 CC -1- FUNCTION: BE (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEDOWN IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ENRICHED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/ OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 CC
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 CC
 CC EMBL; D26509; BA05515.1; -
 CC InterPro; IPR001225; FA_desaturase.
 CC Pfam; PF00487; FA_desaturase; 1.
 CC Prodom; PD001081; FA_desaturase; 1.
 CC Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 CC Transmembrane.
 KW TRANSMEM 52
 FT TRANSMEM 213 72 POTENTIAL.
 FT TRANSMEM 236 256 POTENTIAL.
 FT DOMAIN 97 101 POTENTIAL.
 FT DOMAIN 133 137 HISTIDINE BOX 1.
 FT DOMAIN 300 304 HISTIDINE BOX 2.
 FT HISTIDINE BOX 3.
 SQ SEQUENCE 379 AA; 44149 MW; 872212121AB02E1B2 CRC64;

Query Match 5.0%; Score 146.5; DB 1; Length 379;
Best Local Similarity 23.0%; Pred. No. 0.0001;
Matches 85; Conservative 43; Mismatches 158; Indels 83; Gaps 22.

QY 106 PLNQLVEDPRALQHAEDMKLEFDSPTFFAFLLCHILAMLEYLAMLLYLGLGQWPSAL 165
Db 40 PKHGWAVDPLRSLSYVVRV-----LFAVLLIG-LTAIDMSLWLPYV---W----- 82
QY 166 AAFLLATSAQSSWC---LQHDLGHASIFKKSWMNHNVAQEFYMGOLKGFSAHWNFFRHO 222
Db 83 -----AAGTGFMAIVGLGHDCGHGFSFSDQLNNVGHILHSAIL-VPRHGRIISHKH 136
QY 223 HAKNIFPKRDPVAVPVFLGSSSEYEGKKRRY---LPRNQCHLXFLFLGP----- 272
Db 137 HONHGNVEDESVMRPEKLY--NKVGYSTKRLRKIKIFPLLATPRMLMKRSKSGSH 194
QY 273 -PLLLTVNEFVEMLAYMLV-CMQW-----ADLLMAASFARFSLSDPYGPGVLLFPA 326
Db 195 NPVSGL--FPRHKKVYVYSTLQWVMAALLYLCTAGCS--LDMFKIYAP-YLLEVA 248
QY 327 VVLESHMEFWITQNMHIKFEIGHEKHKRDWVSSQL-----AATCNVEPSLFTNMFSGH 379
Db 249 -----WDFEVTYLLHH-----HGYEKKLPWYKGRKMSYLRGGLTTPYRDGLGFNN-IHHD 296
QY 380 LNFQIEHLEFPRPRHNSRVAPLVKSLCAKGLSEYK-----PLFLATVDIVSLSK- 433
Db 297 IGFVTHHLEFPQIFPHHLEATKRAKRPVLYGK--YREPKKSGPIPF-HLVKDLTRSKQD 353
QY 434 -----SGDI 437
Db 354 HYVSDGEI 362

RESULT 5
FD31.BRANA STANDARD: PROT: 377 AA.
AC P46311.BRANA
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.99.-)
DE (version 1).
GN FAD3.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed.
KA MEDLINE=94302147; PubMed=8029334;
RA Yedav N.S., Wierzbicki A., Aegeerter M., Caster C.S., Perez-Grau L.,
RA Kinney A.J., Hitz W.D., Booth J.R., Jr., Schweiger B., Stecca K.L.,
RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
RA Feldmann K.A., Pierce J., Browse J.;
RT Cloning of higher plant omega-3 fatty acid desaturases.";
RL Plant Physiol. 103:467-476(1993).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC
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[illegible]

DR EMBL; AD12198; CAA18198.1; -
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desaturase; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
KW Transit peptide.
FT TRANSIT 1 69 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 70 448 OMEGA-6 FATTY ACID DESATURASE.
FT DOMAIN 171 175 HISTIDINE BOX 1.
FT DOMAIN 207 211 HISTIDINE BOX 2.
FT DOMAIN 367 371 HISTIDINE BOX 3.
SQ SEQUENCE 448 AA; 51225 MW; C3AC2F828FE8287 CRC64;

Query Match 5.9%; Score 145; DB 1; Length 448;
Best Local Similarity 20.1%; Pred. No. 0.00017;
Matches 70; Conservative 53; Mismatches 136; Indels 90; Gaps 17;

QY 96 LAPEFSQDGLNALDYERFRLHQAADM-----KLDASP-----TFF 135
Db 74 VAP--PSADAEERQDLASYSGRIGEDLPBNYTLKDMDLTKREVEYEDLDKLSVL 131
QY 136 AFLGLHLMAYLA-----WLLIYLPGWVPSALAFILIASQASWCLDHLGHASIFPK 192
Db 132 ISVSTSLGLFEMIAKSPMYLLPLAW-AWTGTAITGEFV-----IGDCAHKSFSK- 180
QY 193 SWNNHVAQKVMQOLKSGFSAH-----WNRHNOHAKNIPIHKQDVTVAPEVLDESSV 248
Db 181 ----NKLVED-IVGTILAEPLVYPERPMFKRKHRIAKIMLVHDTAQQRPYRPEFESSY 236
QY 249 EYGRKKRRRLPYNQOHLTYFLIGP--PLTLVNF-----EENLAIYMLVCM- 292
Db 237 -----MRAIIIFGYGPIRPMLSIAHWMMHFNLRKPRASEVNRVKSISLACEV 283
QY 293 QMADLLMAASFYARFLSYLPFGYGPVGLFEFAVVRLESHMFWIIQMHIFKEIGHEK 352
Db 284 AFWAVGMPILIVYKVGILGWKFMILPMILGYHF-----NMSTFWMHTHTARPHIFKP 334
QY 353 HRDW--VSOLATNCVNERSLFTNMFS---GLNROIEHLHPRMPRHNN 396
Db 335 ADENMAQAQDNGTGHCD---YPSNIEILCHDINHVIHPIHSPIPSYN 380

RESULT 7
FD32_BRANA STANDARD; PRT; 383 AA.
AC P48624;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.99.-)
DN (Version 2).
GN FAD3.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustroids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxId=3708;
RX MEDLINE-93088059; PubMed-1455229;
RA Arondei V., Demieux B., Hwang I., Gibson S., Goodman H.M.,
RA Somerville C.R.;
RT "Map-based cloning of a gene controlling omega-3 fatty acid
RT desaturation in Arabidopsis.";
RL Science 258:1333-1355(1992).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBT BOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC REESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.

```

CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC -----
CC EMBL: L01418; AAA32994.1; -.
CC InterPro: IPR001225; FA_desaturase.
CC Pfam: PF00487; FA_desaturase; 1.
CC ProDom: PD001081; FA_desaturase; 1.
CC Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
CC Transmembrane
CC TRANSMEM 53 73 POTENTIAL.
CC TRANSMEM 210 220 POTENTIAL.
CC TRANSMEM 234 254 POTENTIAL.
CC DOMAIN 98 102 HISTIDINE BOX 1.
CC DOMAIN 134 138 HISTIDINE BOX 2.
CC DOMAIN 301 305 HISTIDINE BOX 3.
CC SEQUENCE 383 AA; 43936 MW; DAD7C3A6FA12826A CRC64;

Query Match 5.9%; Score 144; DB 1; Length 383;
Best Local Similarity 23.8%; Pred. No. 0.00017;
Matches 92; Conservative 51; Mismatches 148; Indels 96; Gaps 26;

QY 100 EPSPDGP LNQVLEDFRALHQAEDMKLEFASP-TFFAFLLGHLIAEVLAMLLIY----- 154
DB 24 DPSQAPFEK---IGDIR-----RAIKRHGVKSPKSMKYTRDFVAVALAMAAVYFDSW 76
QY 155 LIGP-GWPSAL---AAPTILASQASQSMCLQHDGHSI-----FKKSMNHVAKQVMO 206
DB 77 FLMPLYVAVAGTLEMAIFVLG-----HDCGHSFSQIRPLINLVGHILHSIL-- 124
QY 207 LKGSAMWNRFRHONHAKPRIFHKDPDYVAVPVLGSESVYEGKKRRY---LRYNOO 263
DB 125 ---VRYGWRHISRTNH---QNHGHVENESWVPRDEKLKYLPRSTMLRYTVPLRLMAY 179
QY 264 HLXFFLIGP-----PLLT-LVNEEVENLALMLVCMQADLMAAFYARFF---LSY 311
DB 180 PLYLWRSPEKSGSHENPYSSLFAPSERKLTATSTTC--MSIML-ATLYVLSFLVDPTVY 236
QY 312 LPRYGAVGVLLFPAVAVRVLESHEFWITQNMNHIREKIGCHEKNRWVSQI-----AAF 364
DB 237 LKTYGVPII--FVM-----WDAVTYLLNH-----HGNDKLPWYRGKEMSTLRGGLT 283
QY 365 CNEPSLFTWESGHLNFOIEHNLFRPRRNYSRVAPLKEST-CAKHGLS-YEVRPILT 422
DB 284 IDROYGIFNN-IHNDIGTAVIHHLRPOIRPNH-----LYDATRAAKHVLGRTYRBPKTS 336
QY 423 ALVDI-----VRSKK-----SGDI 437
DB 337 GAIRPIHVESIVASIKKHUYSDTGD 363

RESULT 8
FD61-SOYBN STANDARD; PRT; 387 AA.
AC P48630;
DT 01-FEB-1996 (rel. 33, Created)
DT 01-FEB-1996 (rel. 33, Last sequence update)
DT 01-MAR-2002 (rel. 41, Last annotation update)
DE Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 1
DE (EC 1.14.99.-).
GN FAD2-1.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatothya; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OC NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=96151506; PubMed=8587990;
RA Heppard E.P., Kinney A.J., Stecca K.L., Miao G.H.;
RT "Developmental and growth temperature regulation of two different
RT microsomal omega-6 desaturase genes in soybeans.";
RL Plant Physiol. 110:311-319(1996).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC CYCLOHOME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN DEVELOPING SEEDS.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: I43920; AAB00859.1; -.
CC InterPro: IPR001225; FA_desaturase.
CC Pfam: PF00487; FA_desaturase; 2.
CC ProDom: PD001081; FA_desaturase; 1.
CC Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
CC Transmembrane
CC TRANSMEM 54 74 POTENTIAL.
CC TRANSMEM 87 107 POTENTIAL.
CC TRANSMEM 121 141 POTENTIAL.
CC TRANSMEM 183 203 POTENTIAL.
CC TRANSMEM 227 247 POTENTIAL.
CC TRANSMEM 251 271 POTENTIAL.
CC DOMAIN 109 113 HISTIDINE BOX 1.
CC DOMAIN 145 149 HISTIDINE BOX 2.
CC DOMAIN 319 323 HISTIDINE BOX 3.
CC SEQUENCE 387 AA; 44662 MW; 49068805C2A1AC31 CRC64;

Query Match 5.9%; Score 144; DB 1; Length 387;
Best Local Similarity 19.7%; Pred. No. 0.00017;
Matches 68; Conservative 52; Mismatches 122; Indels 104; Gaps 17;

QY 127 LFDASPTFAFLIGHIL--AMEVLAMLLIYLLGCPWPSALAFILASQASQSMCLQHD 184
DB 70 IFYIAVTFE-----HLRQPSLAMPILVYL-QGGLTGV-----WYIAIEC 111
QY 185 GHAISIFKSMNHVAKQVMOGLGFSNH-----WNNFRFGQNH-----KPIIFH 230
DB 112 GHRASFRTQWVDVV-----GLTLHSTLLVPRFSWKISHRRHSNTGSLQDEVEY 162
QY 231 KDPDYVA-----PVFL-LGSSVEYGGKKRRRLPY----- 260
DB 163 PKPKRSVAVFSKYLNNPLGRAVSLVTLTGMPYLAFNVSGRPDVSFAHHYAPLTS 222
QY 261 NOOHLYFFLIGPRLITLVNEEVENLALVCMQADLMAAFYARFLSYLPYGVGCV 320
DB 223 NRERLITYSDVAL-----FSYTSILYVAITLK--GLVM-----LLCYGVPELL 264
QY 321 LLEFVAVRVLESHEFWITQNMNHIREIGH--EKHDWVSSQIAATCNEPSLFTWESG 378
DB 265 IV-----NGFLVITTYLQHTHFALPHYDSSEWDMKGLAL-ATMDRDYGLMKVFNH 314

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OY 279 HLNFOIHHLPKPRRHNSTRVAPLVKSLCAGSLSTVEKPELRL 424
 DB 315 ITDTHVAHLESTMPHYHAMEATNAIKPIGLGEY-YOFDDTPRYKAL 359

RESULT 9
 FD6C_BRANA STANDARD: PRT: 443 AA.

AC 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.99.-).
 OS Brassica napus (Rape).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 CC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:
 CC eucotsids II: Brassicales: Brassicaceae, Brassica.
 OK NCBI_TaxID=3708;

RA SEQUENCE FROM N.A.

RP TISSUE=Seed;

RX MEDLINE=94345008; PubMed=8066133;
 RA Hatz W.D., Carlson T.J., Booth J.R. Jr., Kinney A.J., Stecca K.L.,
 Yadav N.S.;

RT Cloning of a higher-plant plastid omega-6 fatty acid desaturase cDNA
 and its expression in a cyanobacterium.";

RL Plant Physiol 105:635-641(1994).

CC FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.

CC PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.

CC SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).

CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).

CC AND/OR BE INVOLVED IN METAL ION BINDING.

CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

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 or send an email to license@sib-sib.ch).

CC EMBL: L29214; AAA50157.1; -
 InterPro: IPR001225; FA_desaturase.

DR Pfam: PF00487; FA_desaturase; 1.

DR PRODOM: PD001081; FA_desaturase; 1.

KM Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;

KN Transf. peptidase.

FT TRANSIT 1 64 CHLOROPLAST (BY SIMILARITY).

FT CHAIN 65 443 OMEGA-6 FATTY ACID DESATURASE.

FT DOMAIN 166 170 HISTIDINE BOX 1.

FT DOMAIN 202 206 HISTIDINE BOX 2.

FT DOMAIN 362 366 HISTIDINE BOX 3.

FT SEQUENCE 443 AA; 50755 MW; 27344B3AF2781D8 CRC64;

Query Match 5.8%; Score 142; DB 1; Length 443;
 Best Local Similarity 20.8%; Pred. No. 0.00029;
 Mismatches 67; Conservative 50; Mismatches 137; Indels 68; Gaps 14;

DB 103 ODGPINQVLEDFRAHQAEKMDKIDASTPFAFLIGHIIMEVIA---WIIYLLGPG 159
 DB 94 ODLPNWTLMKIDTLPKEVPEIDVYKAMSVLIYSTALGUMTAKAPWILFLAN-A 152
 OY 160 WPSALAAFLIATISQAQSCWCLQHDHGLASIFKRSWMNHYAKQFVKGQKGSFAHW---W 215
 DB 153 WTGTAVTGFV-----IGHDCARSKSPK---NKIYED-IVGTIAFLPLVYPRPW 198

OY 216 NERRHOHAKPNIEHKDPQVTAPEVFLGESSVEYKRRRLPYNOOHLFPLGP--P 273
 DB 199 RFKDRHAKTNMLVDHTAMQVPPEEPDSSPY-----LKAIIIEYGIIR 245
 OY 274 LLLTVNF-----EVENIAYMLVCM-QNADLLMAAFARFELSLDFYVGP 319
 DB 246 WLSTAHVWNNHFWLRFKRPSEVNRKVLACVAFAPAGWVPLLKYGVGLGWKFMMPW 305
 OY 320 VLLFEVAVRLESFHWFWITONHIFKEIGHEKHDM--VSSOLATGVNPEPSLTNMF 377
 DB 306 LGYIF-----WMSTFMVHTHTAPHLPFKRADMNAQAQINGYHCD---YPSMIE 353
 OY 378 ---GHNLQIEHHLFPPMRHN 396
 DB 354 ILCHDIVHPIPHHSIPRPSYN 375

RESULT 10
 FD6E_ARATH STANDARD: PRT: 383 AA.

AC 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Omega-6 fatty acid desaturase, endoplasmic reticulum (EC 1.14.99.-)

DE (Delta-12 desaturase).

GN FAD2 OR AT3G12120 OR T2387.6 OR T21B14.6 OR T21B14.107.

OS Arabidopsis thaliana (Mouse-ear cress).

CC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:

CC eucotsids II: Brassicales: Brassicaceae; Arabidopsis.

OK NCBI_TaxID=3702;

RA SEQUENCE FROM N.A.

RP MEDLINE=94176997; PubMed=7907506;

RX Okuley J., Lightner J., Feldmann K.A., Yadav N., Lark E., Browse J.;

RT "Arabidopsis FAD2 gene encodes the enzyme that is essential for
 polyunsaturated lipid synthesis.";

RT Plant Cell 6:147-158(1994).

CC [2]

CC SEQUENCE FROM N.A.

RP STRAIN=CV, COLUMBIA;

RX MEDLINE=21016720; PubMed=11130713;

RA Salanoubat M., Lemcke K., Rieger M., Ansgore W., Unseld M.,
 Fatmann B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,
 Delesny M., Boutry M., Grivell L.A., Maché R., Puigdemecq P.,
 Del Simone V., Choise N., Altgenave F., Robert C., Brothier P.,
 Wincker P., Catolico L., Weissbach J., Saurin W., Quelier F.,
 Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Bees V.,
 Wurmbech E., Drzomak H., Erile H., Jordan R., Brandt P., Nyakatura G.,
 Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simionati B.,
 Conrad A., Hornischer K., Kauer G., Loehner T., H., Nordstiek G.,
 Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
 Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
 Cooke R., Landie M., Berger-Llauro C., Purnelle B., Masuy D.,
 De Haan M., Maarse A.C., Alcazar J.-P., Cottet A., Cassacubeta E.,
 Montfort A., Argirou A., Flores M., Jigouri R., Vitale D.,
 Manhaupt G., Haase D., Schoof H., Rood S., Zaccaria P., Mekes H.-W.,
 Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 Roycey T., Rizzo M., Wallis A., Ulterback T., Fujii C.Y., Shea T.P.,
 Cressy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
 Pal G., Miltscher J., Sellers P., Gill J.E., Feldjanyum T.V.,
 Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,

RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasaomoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
RA Matanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana.";

RL Nature 408:820-822(2000).

CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES

CC THE SECOND DOUBLED BOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,

CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE

CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS

CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER

CC PHOSPHOLIPIDS.

CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.

CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.

CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTRAIN THE ACTIVE SITE

CC AND/ OR BE INVOLVED IN METAL ION BINDING.

CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

CC -----

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CC -----

CC EMBL: L26296; AAA32782.1; -

DR EMBL: AP002063; BAB01960.1; -

DR EMBL: AC069473; AAG51042.1; -

DR InterPro: IPR001225; FA_desaturase.

DR Pfam: PF00487; FA_desaturase; 2.

DR ProDom: PD001081; FA_desaturase; 1.

KN Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;

KN Transmembrane.

FT TRANSMEM 56 76 POTENTIAL.

FT TRANSMEM 117 137 POTENTIAL.

FT TRANSMEM 179 199 POTENTIAL.

FT TRANSMEM 225 245 POTENTIAL.

FT TRANSMEM 252 272 POTENTIAL.

FT DOMAIN 105 109 HISTIDINE BOX 1.

FT DOMAIN 141 145 HISTIDINE BOX 2.

FT DOMAIN 315 319 HISTIDINE BOX 3.

SO SEQUENCE 383 AA; 44047 MW; 8815ADD2D3BBC982 CRC64;

Query Match 5.8%; Score 141; DB 1; Length 383;

Best Local Similarity 21.1%; Pred. No. 0.00029;

Matches 78; Conservative 48; Mismatches 141; Indels 102; Gaps 18;

132 PTFPAFLGHTL-----AMEVLAMLLIYLGGWPSLAFLIAIS 173

DB 50 PRSFSYLSLDIIISCFYVATVYFSLDLPOLSYLAWPL-YWACCGCVLTGI----- 100

QY 174 QAQSCWLOHDHGASIFKKSMMNH---VAQKVMGQLKGSFAHWNFRHQHAKPNIF 229

DB 101 ---WVAHEGCHAFSDYQWMDYGLLFHSFL--VYYS---WKSXHRHHSNTGSL 151

QY 220 HKDPDYVAVYFPLGESSV---EYGGKKRRLPRNOOHLFFPLGLPRLTLVNEVENLAY 267

DB 152 ERD-----EYFVPRKQSAIKWTKLNNPLGRIMLTVQFPLGRL--YLAFVNSGRPY 203

QY 288 -----MLVCMQWADLL-----WASFYARFLSYLPPYGVGV 320

DB 204 DGFACHFPPNAPLYNDRERLQIYISDAGILAWCFGLYRYAA---AQGASMKICLYGP- 258

QY 321 LLFFAVAVYLSHFWITQGMNHIPKEIGH--EKHNDVSSQLATCVESLSLTNNFSG 378

DB 259 LLIVAVAYLVL-----ITYLQHTPSLSPLHYDSSEMDWLRGML-ATVYRDYGILAKKFFHN 310

QY 379 HLNFQIEHILFPRMRRNYSRVAPLVKSLCAKHGSLYEVEKPLTAL-----VDIVR 429

DB 311 ITDTFHAHHLFTMPHYNAMEATKAIKPIIGDY-YQFDGTPWYVAMRYAKDCIYVEPDR 369

QY 430 SLRKSQDIW 438

DB 370 EGDKKGYW 378

RESULT 11

DESA_SYNT3

ID DESA_SYNT3

AC P20388;

DT 01-FEB-1991 (rel. 17, Created)

DT 01-FEB-1991 (rel. 17, Last sequence update)

DT 01-MAR-2002 (rel. 41, Last annotation update)

DE Fatty acid desaturase (EC 1.14.99.-) (Delta 12 desaturase).

GN DESA OR SLR1350.

OS Synechocystis sp. (strain PCC 6803).

OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.

OX NCBI_Taxid=1148;

OX NCBI_Taxid=1148;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90370121; PubMed=2118597;

RA Wada H., Gombo Z., Murata N.;

RT "Enhancement of chilling tolerance of a cyanobacterium by genetic

RT manipulation of fatty acid desaturation.";

RL Nature 347:200-203(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97061201; PubMed=8905231.

RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

RA Hoshijima N., Hirosewa M., Sugitani M., Sasamoto S., Kimura T.,

RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,

RA Okumura S., Shimp S., Takeuchi C., Wada T., Matanabe A.,

RA Yamada M., Yasuda M., Tabata S.;

RT "Sequence analysis of the genome of the unicellular cyanobacterium

RT Synechocystis sp. strain PCC6803. II. Sequence determination of the

RT entire genome and assignment of potential protein-coding regions.";

RL DNA Res. 3:109-136(1996).

CC -1- FUNCTION: CAN INTRODUCE A SECOND CIS DOUBLE BOND AT THE DELTA 12

CC POSITION OF FATTY ACID BOUND TO MEMBRANE GLYCEROLIPIDS. THIS

CC ENZYME IS INVOLVED IN CHILLING TOLERANCE BECAUSE THE PHASE

CC TRANSITION TEMPERATURE OF LIPIDS OF CELLULAR MEMBRANES DEPENDS ON

CC THE DEGREE OF UNSATURATION OF FATTY ACIDS OF THE MEMBRANE LIPIDS.

CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

CC -----

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CC -----

CC EMBL: X53508; CAA37584.1; -

DR EMBL: D90912; BAA18169.1; -

DR PIR: S11519; S11519.

DR InterPro: IPR001225; FA_desaturase.

DR Pfam: PF00487; FA_desaturase; 1.

DR ProDom: PD001081; FA_desaturase; 1.

DR PROSITE: PS00574; FATTY ACID DESAT_2; 1.

KN Oxidoreductase; Fatty acid biosynthesis; Membrane; Complete proteome.

FT DOMAIN 90 94 HISTIDINE BOX 1.

FT DOMAIN 126 130 HISTIDINE BOX 2.

FT DOMAIN 287 291 HISTIDINE BOX 3.

SO SEQUENCE 351 AA; 40495 MW; 85DBBE8341F73F77 CRC64;

Query Match 5.8%; Score 140.5; DB 1; Length 351;

Best Local Similarity 22.3%; Pred. No. 0.00029;

Matches 81; Conservative 44; Mismatches 154; Indels 85; Gaps 17;

90 PLLIGELAPEPSQDGPL-NAQVDEDFRALHQAEDMKLFDPASPTFPALV--LGIH----- 142


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Db      6 PLETPVTPSPNP--DRPIADLKLDIITKPECEFEK---ASKAMASVILITGATAVGY 60
QY      143 LAMEVIALMLIYLGRGVWPSALA--AFILAIISOQSWCLOHDLGASIFKSKWNHVA 199
Db      61 LGITITPWP---YCLPITITWGTALGAFVVG-----HDCGRSRAKRWINDLV 107
QY      200 QKFWGQGLKGSFAMWNNRHFQHNKAPNIFHKDP--DYVAAPVFLGSESVYGGKKRRY 257
Db      108 GHIAFAPLI-YPFHSMRLIHDHHLHTNRIEVDNAMPWSEVAFQASPAIV----- 157
QY      258 LYNNOOHLYEFLIGPPL-----LFLVNFVEENLAY-----MLVCMQMDLLWA 300
Db      158 -----RLEFRAIRGPFWMTGSIFFHWSLMHFKLSNFQDRNKKLSIAVYFLAALAP 211
QY      301 ASFYANFSLYLPEYGVDPVLLFVAVAVLESHPFVMTQNNHLPKEIGEHKRDW--VS 358
Db      212 ALITITGVWGFVKFVLMVLYVHF-----WMSTFTYVHHTIPRIRPAADWSAAE 262
QY      359 SOLAATCNVPSLFTNNWPSGHLNFQIEHNLFPFRPHRYSHVADLVKSLCAKHS-LSEYV 417
Db      263 AQNLGVHCDYPRWVEVLCHDNLNVAIRHLSVALPSYN-----LALAGSLKENW 312
QY      418 KPPL 421
Db      313 GPPL 316

RESULT 12
ID      N1AL_SQYBN STANDARD: PRT: 886 AA.
AC      P54233;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DE      01-OCT-1996 (Rel. 34, last annotation update)
GN      Inducible nitrate reductase 1 (EC 1.6.6.1) (NR).
OS      Glycine max (soybean).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC      Eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX      NCBI_TaxID=3847;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=CV. WILLIAMS; TISSUE=leaf;
RX      MEDIANP=96123229; PubMed=8534848;
RA      Wu S., Lu Q., Kritz A.L., Harper J.E.;
RT      Identification of cDNA clones corresponding to two inducible nitrate
RT      reductase genes in soybean: analysis in wild-type and nrl mutant.";
RL      Plant Mol. Biol. 29:491-506(1995).
CC      1- FUNCTION: NITRATE REDUCTASE IS A KEY ENZYME INVOLVED IN THE FIRST
CC      STEP OF NITRATE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.
CC      1- CATALYTIC ACTIVITY: NADH + nitrate = NAD(+) + nitrite + H(2)O.
CC      1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
CC      AND ONE MOLYBDENUM ATOM.
CC      1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC      1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC      N-TERMINAL DOMAIN.
CC      1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC      C-TERMINAL DOMAIN.
CC      1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC      C-TERMINAL DOMAIN.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      EMBL: L23854; AAA96727.1; -
CC      HSPSP, P17571; 2CND
DR      InterPro: IPR001199; Cyt_B5_
DR      InterPro: IPR001834; Cyt_B5_reductase.

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DR      InterPro: IPR000572; Euk_oxidored_molyb.
DR      InterPro: IPR001709; Flavyrid_cyt_redctse.
DR      InterPro: IPR001433; Oxidored_FAD.
DR      Pfam: PF00970; FAD_binding_6; 1.
DR      Pfam: PF00173; heme_1; 1.
DR      Pfam: PF00175; NAD_binding_1.
DR      Pfam: PF00174; oxidored_molyb; 1.
DR      PRINTS: PR00406; CYTBSDTASE.
DR      PRINTS: PR00363; CYTOCHROME5.
DR      PRINTS: PR00407; EUMOPTERIN.
DR      PRINTS: PR00371; FPNCR.
DR      PROSITE: PS00191; CYTOCHROME B5_1; 1.
DR      PROSITE: PS02855; CYTOCHROME B5_2; 1.
DR      PROSITE: PS00559; MOLYBDOPTERIN_EUK; 1.
DR      PROSITE: PS00559; MOLYBDOPTERIN_EUK; 1.
KW      Oxidoreductase; Flavo-protein; FAD; NAD; Heme; Molybdenum;
KW      Nitrate assimilation; Multigene family.
FT      METAL 165 165 MOLYBDENUM-PTERIN (POTENTIAL).
FT      METAL 219 219 MOLYBDENUM-PTERIN (POTENTIAL).
FT      DISULFID 404 404 INTERCHAIN (POTENTIAL).
FT      BINDING 548 548 HEME LIGAND (BY SIMILARITY).
FT      BINDING 571 571 HEME LIGAND (BY SIMILARITY).
SQ      SEQUENCE 886 AA; 99798 MW; C18C73BDE3DB0614 CRC64;

Query Match 5.8%; Score 140.5; DB 1; Length 886;
Best Local Similarity 19.1%; Pred. No. 0.00087;
Matches 74; Conservative 48; Mismatches 119; Indels 147; Gaps 16;

QY      22 TFCWEQIRADPGDKVLVTERRVYDISMAORHPSGRLIGHGAEATDAPAFAPQDL 81
Db      515 TYTMSVRRRNNDASAMITVHGVYDMTRFLKDHHGGDRILLNAGTCTEEFAHISDK 574
QY      82 NEVKKLQPLILIGL-----ADEPSDGC-----PLN-AQVDFRAL----- 118
Db      575 --AKQMLEDRIGELFTTCYNSDSSSNPSVHGRSDTLPDPKEIKVTPMSVALIREK 632
QY      119 -----HOAEDMKLFDSPTFEAFILGHILAMEVIALMLIYLGRGVWPSALAAFIL 170
Db      633 IPCKLIKSTISHDYKLFREGLPDSGLMGLAVGKHI-----FL 671
QY      171 AISOQSWCLO-----HDIGHASIFKSKWNHVAQNF-----VMQ----- 206
Db      672 CVTVDKELCMRAVYPTSSVHEGVYFDLVVYKVGHPFGNGIMSOLDLPLGVSYLD 731
QY      207 LKGSAN--WMNFRHFQHNKAPNIT-----FKKD-DYVAAPV- 240
Db      732 VKPGLGHIEYGRGNFLVHGRKPAFATRLAAGGTTFTYGVAILKDPEDDCEMHVY 791
QY      241 -----FLGSESVYGGKKRR-----YLPNQO 263
Db      792 YANRTEDDILKEELDMARKYRLKWWYVIGRSIREGWEVSQFTESILTEHIPNASP 851
QY      264 HLYEFLIGPPLTLVNFV-----ENLAY 287
Db      852 DTIALTGCP--PMIOFAVQPNLEKLG 877

RESULT 13
ID      F33E_PHAU STANDARD: PRT: 380 AA.
AC      P32291.
DT      01-OCT-1993 (Rel. 27, Created)
DT      01-OCT-1993 (Rel. 27, last sequence update)
DT      01-MAR-2002 (Rel. 41, last annotation update)
DE      Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.99.-)
DE      (Indole-3-acetic acid induced protein Ark1).
GN      Ark1.
OS      Phaseolus aureus (Mung bean) (Vigna radiata).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC      Eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX      NCBI_TaxID=3916;
RN      [1]

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RP SEQUENCE FROM N.A.
RC TISSUE-Hypocotyl;
RA Yamamoto K.T., Mori H., Imaseki H.;
RT "Novel mRNA sequences induced by indole-3-acetic acid in sections of
RL elongating hypocotyls of mung bean (*Vigna radiata*).";
RL Plant Cell Physiol. 33:13-20(1992).
CC -1- FUNCTION: MICROSOMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
CC -1- INDUCTION: BY AUXIN, ETHYLENE AND WOUNDING.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D14410; BAA03306.1; -
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF00487; FA_desaturase; 1.
DR ProDom: PD001081; FA_desaturase; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
KW Transmembrane.
FT TRANSMEM 59 78 POTENTIAL.
FT TRANSMEM 208 231 POTENTIAL.
FT TRANSMEM 238 256 POTENTIAL.
FT DOMAIN 97 101 HISTIDINE BOX 1.
FT DOMAIN 133 137 HISTIDINE BOX 2.
FT DOMAIN 300 304 HISTIDINE BOX 3.
SQ SEQUENCE 380 AA; 43996 MW; 1C005117A8DAE16B CRC64;

Query Match 5.7%; Score 140; DB 1; Length 380;
Best Local Similarity 20.5%; Pred. No. 0.00035;
Matches 77; Conservative 40; Mismatches 124; Indels 134; Gaps 18;

OY 152 LYLILGQWPSALAFILAIISOAGW-----CLOHDLGHASIRKKSMMN 196
DB 52 LSTVLRDYLVTALASALISFNSWFWPLXPAQGTMTALFVLGHDCGHSFSSSKLN 111
OY 197 ---HVAQKRVMGOLKGFSAHWMNFRFHAKRPNIFRKD-----PDVT-- 236
DB 112 SFVGHILHSLILVYNG---WRISHRTIHONHGHVEDESWVPLTEKYKKNLDDMTRM 166
OY 237 -----VAPVELIGSESVYEYGGKKRRRLPYNOQHLYFLIQLRPRLTLVNEVEVNL 266
DB 167 LRYGPPPIRAYPYLYLNNRSP---GKGGSHFNPIYSN-----LESPG-----ERKGV 210
OY 287 YMLVCMQWADLMAAFYARFELS-----YLPYGVGVLLFVAVAVLESHWFWMT 339
DB 211 TSTLC-----WGIYLVSLVLLSLTIGPIFMKLKLYGPV--YLIFVM-----WLFVY 254
OY 340 OMN-----IPKEIGH-----KRDWVYSGDLATQVESPSTLNNFNSGHLN 381
DB 255 YLHHNGTHKLPMYRGQEWYSLAGGLTYVDROYGNIN-----NVNHDITGH----- 300
OY 382 FOLEHHLFPRMRRHNSRVAPLVKSIKANH-----GLSTEVKPFLLALVDIVRSLEKK 433
DB 301 --VIHHLFPOIPHYHLVEATKSAKSVYKGYREPOKSGPLFPHLKLKYLQSIODHFWSD 358
OY 434 SGDI---WLDAYLHQ 445
DB 359 TGDIVYQYQTPKLIHQ 373

RESULT 14
FD3E.SOYBN STANDARD; PRT; 380 AA.
AC P48625;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Omega-3 fatty acid desaturase, endoplasmic reticulum (BC 1.14.99.-).
GN RAD3.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=94302147; PubMed=8029334;
RA Yadao N.S., Wierzbicki A., Aegeerter M., Gaster C.S., Perez-Grau L.,
RA Kinney A.J., Hitz W.D., Booth J.R., Jr., Schweizer B., Stecca K.L.,
RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
RA Feldmann K.A., Pierce J., Browne J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases.";
RL plant Physiol. 103:467-476(1993).
CC -1- FUNCTION: MICROSOMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L22964; AAA61777.1; -
DR PIR: JQ2338; JQ2338.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF00487; FA_desaturase; 1.
DR ProDom: PD001081; FA_desaturase; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
KW Transmembrane.
FT TRANSMEM 55 75 POTENTIAL.
FT TRANSMEM 212 232 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 100 104 HISTIDINE BOX 1.
FT DOMAIN 136 140 HISTIDINE BOX 2.
FT DOMAIN 303 307 HISTIDINE BOX 3.
SQ SEQUENCE 380 AA; 44185 MW; BF80DF93CF4C29D7 CRC64;

Query Match 5.7%; Score 140; DB 1; Length 380;
Best Local Similarity 19.3%; Pred. No. 0.00035;
Matches 62; Conservative 39; Mismatches 100; Indels 120; Gaps 15;

OY 136 AFLGLHAMEVIA-----WLLIYLGPQWPSALAFILAIISOAGWCLQHDIGHA 187
DB 56 SYVLRLDVLVLAALVAALIFHDWMLLMILYCPICGTMTALFVLG-----HDCGHA 105
OY 188 SIFKSKMMN---HVAQKRVMGOLKGFSAHWMNFRFHAKRPNIFRKDP----- 234
DB 106 SFSDSLNLNVGHILHSLI-----VPIHGKRIKRTIHONHGHTEKDESWVPLTEKIT 160

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QY 235 -----VTAPVFLIGSSVYGGKKRRRLPYNOCHLFFELGPELLTL 277
DB 161 KNLDSMTLLRIETVPEPLFVYPIYLFSSNP---GKEGSHNPYSN-----LFPD----- 206
QY 278 VNEVEENLAVMLVCMQWMDLMAASFARFLSY-----LPEYGVPGVILFEVAVRVL 330
DB 207 --SERGIASITLC-----WATMFSLILYLSFTSPBLVLKLYGTP-----YWIFVM-- 251
QY 331 ESHWETWITQNNHKEKGEKHKDM-----VSSQLATGCVNPSLSFTVM 375
DB 252 ---WIDFVYVYLLH---HGHHQKLPWYRGKEMSYLRGLTATVDYDGYMIVNHIDGTH- 303
QY 376 FSGHLNFQIENHLPFMRPRHN 396
DB 304 -----VIHHLFPQIDPHYH 316

RESULT 15
NIAL TOBAC STANDARD; PRT: 904 AA.
AC R11605;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE Nitrate reductase 1 (EC 1.6.6.1) (NRL).
GN NIAL
OS Nicotiana tabacum (common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxId=4097;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=CV. XANTHI; TISSUE=leaf;
RA Vaucheret H., Kronenberger J., Rouze P., Caboche M.;
RT Complete nucleotide sequence of the two homologous tobacco nitrate
RT reductase genes.
RL Plant Mol. Biol. 12:597-600(1989).
CC 1- FUNCTION: NITRATE REDUCTASE IS A KEY ENZYME INVOLVED IN THE FIRST
CC STEP OF NITRATE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.
CC 2- CATALYTIC ACTIVITY: NADH + nitrate = NAD(+) + nitrite + H(2)O.
CC 3- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
CC GROUP IS CALLED CYTOCHROME B-557.
CC 4- ENZYME REGULATION: REGULATED BY THE NITROGEN SOURCE AND CONTROLLED
CC BY THE CIRCADIAN RHYTHM.
CC 5- SUBUNIT: HOMODIMER.
CC 6- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC 7- SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN.
CC 8- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X14058; CAA32216.1; -
DR PTR: S04839; RDNPTT.
DR HSP: P17571; ZCND.
DR Mendel; 1123; NITCA; Nial.1.
DR Interpro: IPR001199; Cyt_B5.
DR Interpro: IPR001834; Cyt_B5_reductase.
DR Interpro: IPR000572; Euk_oxidored_mol.
DR Interpro: IPR001709; Flavpyrid_cyl_reductse.
DR Interpro: IPR001433; Oxidored_cyl.
DR pfam: PF00970; FAD_binding_6; 1.
DR pfam: PF00173; heme_1; 1.

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DR pfam: PF00175; NAD binding; 1.
DR pfam: PF00174; oxidored_mol.
DR PRINTS: PR00406; CYTSRDTASE.
DR PRINTS: PR00363; CYTOCHROME B5.
DR PRINTS: PR00407; EMOPTERIN.
DR PRINTS: PR00371; FPNCR.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00559; MOLYBDOPTERIN_EUK; 1.
KW Oxidoreductase; Flavo-protein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation; Multigene family.
FT METAL 183
FT METAL 237
FT DISULFID 422
FT BINDING 566
FT BINDING 589
SQ SEQUENCE 904 AA; 101907 MW; 85642BDA723EE154 CRC64;

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Query Match 5.7%; Score 138.5; DB: 1; Length 904;
Best Local Similarity 27.1%; Pred. No. 0.0013;
Matches 36; Conservative 16; Mismatches 44; Indels 37; Gaps 4;
QY 11 EGPAQPG-----APLPT-----PCWEQIRAHDPDGD 36
DB 489 EHPYQPNQSGWMAKERHLEISAEAP-PTLKSIPTPFMMTASMYSMSEVRKSSADS 547
QY 37 KMLVIERRVYDIIRMAQRHFGSGRLGHGAGADADAPRAFHODLNFYRKLOPLLIGEL 96
DB 548 AMIVHGHITDARFRLADHFGSDSLINAGHDTCEFDALHSDK--AKKLLERFRIIGEL 605
QY 97 APEEPSQDGPLNA 109
DB 606 LTGTYSDSPEGS 618

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Search completed: October 7, 2002, 11:45:27
Job time: 251 sec

Tue Oct 8 10:29:16 2002

us-09-806-088-3.rsp

Page 12

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 7, 2002, 11:40:51 ; Search time 31.08 Seconds
(without alignments)
2476.922 Million cell updates/sec

Title: US-09-806-088-3
Perfect score: 2437
Sequence: 1 MGVGEGEPGEPGAPGAPL.....DIVRSUKKSGDIMDYLHQ 445

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : SPTEMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2437	100.0	445	09Y500	09Y500 homo sapien
2	2182	89.5	449	11 09JIE7	09JIE7 mus musculu
3	1575.5	64.6	444	4 095864	095864 homo sapien
4	1567.5	64.3	444	11 092122	092122 rattus norv
5	1566.5	64.3	444	11 0920R9	0920R9 mus musculu
6	1410	57.9	454	13 0985W7	0985W7 oncorhynch
7	1401	57.5	454	13 0902E8	0902E8 oncorhynch
8	1376.5	55.8	444	13 09H3G3	09H3G3 homo sapien
9	1359.5	55.8	444	13 09DEX7	09DEX7 brachydantio
10	1338.5	54.9	352	4 060426	060426 homo sapien
11	1328.5	54.5	386	4 096H07	096H07 homo sapien
12	1326.5	54.4	444	13 09DEX6	09DEX6 cyprinus ca
13	1298	53.3	445	13 0902R3	0902R3 rattus norv
14	1298	53.3	447	11 0920R3	0920R3 rattus norv
15	1283	52.6	447	11 0920L1	0920L1 mus musculu
16	1280.5	52.5	444	4 096T10	096T10 homo sapien

17	1279.5	52.5	444	4 060427	060427 homo sapien
18	1279	52.5	447	11 09EPV4	09EPV4 rattus norv
19	1272.5	52.2	444	4 09NRP8	09NRP8 homo sapien
20	1271.5	52.2	444	4 09MYX1	09MYX1 homo sapien
21	1271.5	52.2	444	4 096139	096139 homo sapien
22	1265.5	51.9	444	4 096SV3	096SV3 homo sapien
23	1132.5	46.5	411	4 09Y3X4	09Y3X4 homo sapien
24	627	25.7	168	4 096SV8	096SV8 homo sapien
25	547.5	22.5	520	10 09LEND9	09LEND9 ceratodon p
26	514	21.1	483	10 09LEND0	09LEND0 ceratodon p
27	496.5	20.4	525	10 09ZNM2	09ZNM2 physcomitrel
28	481.5	19.8	457	3 09UVY3	09UVY3 mortierella
29	481.5	19.8	457	3 09HEV4	09HEV4 mortierella
30	481.5	19.8	457	3 09HEV1	09HEV1 mortierella
31	478.5	19.6	457	3 09UVV3	09UVV3 mortierella
32	467.5	19.2	459	10 0944W4	0944W4 pythium irr
33	467	19.2	469	10 092PT8	092PT8 tritlicum ae
34	448	18.4	449	10 082348	082348 arabidopsis
35	447	18.3	449	10 092RP8	092RP8 brassica na
36	444	18.2	467	3 096VC3	096VC3 mucor circi
37	437	17.9	449	10 092RP7	092RP7 arabidopsis
38	432.5	17.7	446	10 092RY9	092RY9 ricinus com
39	428	17.6	448	10 09SAU5	09SAU5 borago offi
40	427	17.5	448	10 004353	004353 borago offi
41	421	17.3	446	10 09FR82	09FR82 borago offi
42	420	17.2	419	10 09SMQ9	09SMQ9 euglena gra
43	414	17.0	458	10 0434G9	0434G9 helianthus
44	391	16.0	456	10 0944W3	0944W3 pythium irr
45	380	15.6	443	5 061388	061388 caenorhabdi

ALIGNMENTS

RESULT 1

09Y500 PRELIMINARY; PRT; 445 AA.

AC 09Y500; 09Y500;

DT 01-NOV-1999 (TEMBLrel. 12, Created)

DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)

DT 01-OCT-2001 (TEMBLrel. 18, Last annotation update)

DE DELTA-6 FATTY ACID DESATURASE (FATTY ACID DESATURASE 3).

GN CYS5RP OR PADS3.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Li W., Metzger M.L., Caskey C.T., Petrukhin K.;

RT "Human retina-specific delta 6 fatty acid desaturase.";

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=20318619; PubMed=10860662;

RA Maguad A., Stohr H., White K., Weber B.H.F.;

RT "cDNA cloning, genomic structure, and chromosomal localization of

RL Genomics 66:175-183(2000).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=RAADOMTOSARCOMA;

RA Strausberg R.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

DR EMBL; AF134404; AAD31282.1; -

DR EMBL; AF084560; AAG23122.1; -

DR EMBL; BC004901; AAH04901.1; -

DR HSSP; P82291; ICXY.

DR InterPro; IPR001199; Cyt_B5.

DR Pfam; PF00173; heme_1.1; -

DR PRINTS; PR00363; CYTOCHROME_B5.

DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.

KM Heme.
SQ SEQUENCE 445 AA: 51145 MW: 7840EF6BE055111D CRC64:

Query Match 100.0%; Score 2437; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 2,3e-213;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGVGEGRPGRPAOPGAPLPFCWEQIRAHQPGDKMLVTERRYDTSRMAORHRR 60
DB 1 MGVGEGRPGRPAOPGAPLPFCWEQIRAHQPGDKMLVTERRYDTSRMAORHRR 60
QY 61 LIGHGADATDAFRAFHODLNFRKFLQPLLLIGELAEPEPSODGPLNAQLVEDFRALHQ 120
DB 61 LIGHGADATDAFRAFHODLNFRKFLQPLLLIGELAEPEPSODGPLNAQLVEDFRALHQ 120
QY 121 AAEQMKLFDAFPTFFAFLLGHITLAMEVLAMLLIYLLGPGWPSALAAFTILASQASQWCL 180
DB 121 AAEQMKLFDAFPTFFAFLLGHITLAMEVLAMLLIYLLGPGWPSALAAFTILASQASQWCL 180
QY 181 QHDIHGASIFKKSMMNHVAOKFVWGOLKGSAAHMMNFRHFOHAKPNIFHKDPDYVAVY 240
DB 181 QHDIHGASIFKKSMMNHVAOKFVWGOLKGSAAHMMNFRHFOHAKPNIFHKDPDYVAVY 240
QY 241 FLIGESSVEYGGKKRRRLPYNOOHLVFFLLIGPPLTLVNFVENLAAYMLVCMQADLLMA 300
DB 241 FLIGESSVEYGGKKRRRLPYNOOHLVFFLLIGPPLTLVNFVENLAAYMLVCMQADLLMA 300
QY 301 ASFAFRLSLDIPYGPVGLLFFVAAYVLESHEMFVWITOMNHIPKEIGEHKRDWVSSQ 360
DB 301 ASFAFRLSLDIPYGPVGLLFFVAAYVLESHEMFVWITOMNHIPKEIGEHKRDWVSSQ 360
QY 361 LAATCNVPSLFTNWFSGHLNFQIEHHLFPRMRHNSRVAPLVKSLCAKKGSLSEYKPF 420
DB 361 LAATCNVPSLFTNWFSGHLNFQIEHHLFPRMRHNSRVAPLVKSLCAKKGSLSEYKPF 420
QY 421 LTAAYDIYRSLSKSGDIWLDAYLHQ 445
DB 421 LTAAYDIYRSLSKSGDIWLDAYLHQ 445

RESULT 2
Q9JUE7 PRELIMINARY; PRT; 449 AA.
AC Q9JUE7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE BRAIN CDNA, CLONE MNCB-0629, SIMILAR TO HOMO SAPIENS DELTA-6 FATTY ACID DESATURASE (CYB5RP) MRNA.
GN FADS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from mouse brain cDNA library made by oligo-capping method."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: A0041560; BAA95044.1; -.
DR HSP: P04166; IAMP.
DR MGD: MG1:1928740; Fads3.
DR InterPro: IPR001199; Cyt.B5.
DR PRINTS: PR00363; CYTOCHROME5.
DR PROSITE: PSS0255; CYTOCHROME_B5_2; 1.
KM Heme.
SQ SEQUENCE 449 AA: 51497 MW: 6FD874EC8C07750B CRC64:

Query Match 89.5%; Score 2182; DB 11; Length 449;
Best Local Similarity 89.3%; Pred. No. 3.6e-190;
Matches 401; Conservative 11; Mismatches 33; Indels 4; Gaps 1;

QY 1 MGVGE-----PGRGPAPGAPLPFCWEQIRAHQPGDKMLVTERRYDTSRMAORHRR 56
DB 1 MGVGEGRPGRPAOPGAPLPFCWEQIRAHQPGDKMLVTERRYDTSRMAORHRR 60
QY 57 GGSRLIGHGAEDATDAFRAFHODLNFRKFLQPLLLIGELAEPEPSODGPLNAQLVEDFR 116
DB 61 GGSRLIGHGAEDATDAFRAFHODLNFRKFLQPLLLIGELAEPEPSODGPLNAQLVEDFR 120
QY 117 ALHQAPADMKLPDASPFFAFLLGHITLAMEVLAMLLIYLLGPGWPSALAAFTILASQASQ 176
DB 121 ALHQAPADMKLPDASPFFAFLLGHITLAMEVLAMLLIYLLGPGWPSALAAFTILASQASQ 180
QY 177 SWCLOHDLGASIFKKSMMNHVAOKFVWGOLKGSAAHMMNFRHFOHAKPNIFHKDPDYV 236
DB 181 SWCLOHDLGASIFKKSMMNHVAOKFVWGOLKGSAAHMMNFRHFOHAKPNIFHKDPDYV 240
QY 237 VAPYFLIGESSVEYGGKKRRRLPYNOOHLVFFLLIGPPLTLVNFVENLAAYMLVCMQAD 296
DB 241 VAPYFLIGESSVEYGGKKRRRLPYNOOHLVFFLLIGPPLTLVNFVENLAAYMLVCMQAD 300
QY 297 LMAASFYARFSLDIPYGPVGLLFFVAAYVLESHEMFVWITOMNHIPKEIGEHKRDW 356
DB 301 LMAASFYARFSLDIPYGPVGLLFFVAAYVLESHEMFVWITOMNHIPKEIGEHKRDW 360
QY 357 VSSOLAATCNVPSLFTNWFSGHLNFQIEHHLFPRMRHNSRVAPLVKSLCAKKGSLSE 416
DB 361 ASSOLAATCNVPSLFTNWFSGHLNFQIEHHLFPRMRHNSRVAPLVKSLCAKKGSLSE 420
QY 417 VKPFLTAAYDIYRSLSKSGDIWLDAYLHQ 445
DB 421 VKPFLTAAYDIYRSLSKSGDIWLDAYLHQ 449

RESULT 3
O95864 PRELIMINARY; PRT; 444 AA.
AC O95864;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE (FATTY ACID DESATURASE 2).
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99085046; PubMed=9867867;
RA Cho K.P., Nakamura M.T., Clarke S.D.;
RT "Cloning, expression, and nutritional regulation of the mammalian Delta-6 desaturase."
RL J. Biol. Chem. 274:471-477(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=20318619; PubMed=10860662;
RA Margharit A., Stohr H., White K., Weber B.H.F.;
RT "Magna cloning, genomic structure, and chromosomal localization of three members of the human fatty acid desaturase family."
RL Genomics 66:1175-183(2000).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: AF126799; AAD20018.1; -.
DR EMBL: AF084559; AAG23121.1; -.
DR HSP: P00171; IMD8.
DR InterPro: IPR001199; Cyt.B5.
DR Pfam: PF00173; heme.1; 1.
DR PRINTS: PR00363; CYTOCHROME5.
DR PROSITE: PSS0255; CYTOCHROME_B5_2; 1.

Query Match 64.6%; Score 1575.5; DB 4; Length 444;
 Best Local Similarity 62.6%; Pred. No. 5,3e-135;
 Matches 279; Conservative 63; Mismatches 101; Indels 3; Gaps 2;

KW Heme. 444 AA; 52259 MW; F65CE58076961A7A CRC64;
 SQ SEQUENCE

1 MGVGEGEPREGRPAQAPLPTEFCWBOIRANDOPGDKMLVTERRYDYSRAQNRHPCGRS 60
 1 MGKGNQGG--EGAEERVSVPYTSWGEIQKMRTRDRLVTDKRYNITKMSIQHPGGR 58
 1 LGHNGEDATDAFRAPHODINFRKFLQPLILGELAPEEPSODGPLMAOLVEDFRALHQ 120
 59 VIGHYSEDATDAFRAPHODINFRKFLQPLILGELAPEEPSODGPLMAOLVEDFRALHQ 118
 61 AEDMKLPDASPTFFPAFLGHIIAMVYLAAMLLIYLPGWVPSALAAFIATLSQAQSWCL 180
 119 TAEEMNLFKTNHVFLLNHLITLSTIAMFTYFEGKNGMIPYITATVATLSQAQSWCL 178
 119 QHDGHSIFKSSWMNHVAQKFEYMGOLKGFSAHMMNFRHONHAKPNIFHKDPDYVAPV 240
 119 QHDGHSIFKSSWMNHVAQKFEYMGOLKGFSAHMMNFRHONHAKPNIFHKDPDYVAPV 238
 241 FLIGE--SSVEYGGKKRRYLPYNOQHLYFELIGPRLITLVNEFVENLAVLYCMQADLW 299
 239 FVLGEWQPLEYGGKKRLLPYNOQHLYFELIGPRLITLVNEFVENLAVLYCMQADLW 298
 300 AAFYARFELSYLPFGYGVPLLEFYAVVYLSHMFVWITQNMHTPKRIGHEKHHDVSS 359
 299 AAFYARFELSYLPFGYGVPLLEFYAVVYLSHMFVWITQNMHTPKRIGHEKHHDVSS 358
 360 QLATCANEPSLFTNMFSGHINFOIEHNLFPKPRHNSRYAPLVKSLCAHGLSYEVK 419
 359 QLATCANEPSLFTNMFSGHINFOIEHNLFPKPRHNSRYAPLVKSLCAHGLSYEVK 418
 420 FLTALVDIVSLKSGDIDWDAYLHQ 445
 419 LTRALDILVSLKSGELMDAYLHK 444

RESULT 4
 092122 PRELIMINARY; PRT; 444 AA.
 AC 092122;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE DELTA-6 FATTY ACID DESATURASE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE DAWLEY; TISSUE=LIVER;
 RX MEDLINE=99160394; Pubmed=10049752;
 RA Aki T., Shimada Y., Inagaki K., Higashimoto H., Kawamoto S.,
 RA Shiojima S., Ono K., Suzuki O.;
 RT "Molecular cloning and functional characterization of rat delta-6
 RT fatty acid desaturase";
 RL Biochem. Biophys. Res. Commun. 255:575-579(1999).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AB021980; BAA75496.1; -.
 DR HSSP; P00171; 1CYO.
 DR InterPro; IPR001199; Cyt_B5.
 DR Pfam; PF00173; heme_1; 1.
 DR PRINTS; PR00363; CYTOCHROME_B5.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 444 AA; 52380 MW; D9AEOC7AF499A1AE CRC64;

Query Match 64.3%; Score 1567.5; DB 11; Length 444;
 Best Local Similarity 62.8%; Pred. No. 2.8e-134;
 Matches 280; Conservative 63; Mismatches 100; Indels 3; Gaps 2;

KW Heme. 444 AA; 52387 MW; 7615D17024D3B771 CRC64;
 SQ SEQUENCE

1 MGVGEGEPREGRPAQAPLPTEFCWBOIRANDOPGDKMLVTERRYDYSRAQNRHPCGRS 60
 1 MGKGNQGG--EGAEERVSVPYTSWGEIQKMRTRDRLVTDKRYNITKMSIQHPGGR 58
 1 LGHNGEDATDAFRAPHODINFRKFLQPLILGELAPEEPSODGPLMAOLVEDFRALHQ 120
 59 VIGHYSEDATDAFRAPHODINFRKFLQPLILGELAPEEPSODGPLMAOLVEDFRALHQ 118
 61 AEDMKLPDASPTFFPAFLGHIIAMVYLAAMLLIYLPGWVPSALAAFIATLSQAQSWCL 180
 119 TAEEMNLFKTNHVFLLNHLITLSTIAMFTYFEGKNGMIPYITATVATLSQAQSWCL 178
 119 QHDGHSIFKSSWMNHVAQKFEYMGOLKGFSAHMMNFRHONHAKPNIFHKDPDYVAPV 240
 119 QHDGHSIFKSSWMNHVAQKFEYMGOLKGFSAHMMNFRHONHAKPNIFHKDPDYVAPV 238
 241 FLIGE--SSVEYGGKKRRYLPYNOQHLYFELIGPRLITLVNEFVENLAVLYCMQADLW 299
 239 FVLGEWQPLEYGGKKRLLPYNOQHLYFELIGPRLITLVNEFVENLAVLYCMQADLW 298
 300 AAFYARFELSYLPFGYGVPLLEFYAVVYLSHMFVWITQNMHTPKRIGHEKHHDVSS 359
 299 AAFYARFELSYLPFGYGVPLLEFYAVVYLSHMFVWITQNMHTPKRIGHEKHHDVSS 358
 360 QLATCANEPSLFTNMFSGHINFOIEHNLFPKPRHNSRYAPLVKSLCAHGLSYEVK 419
 359 QLATCANEPSLFTNMFSGHINFOIEHNLFPKPRHNSRYAPLVKSLCAHGLSYEVK 418
 420 FLTALVDIVSLKSGDIDWDAYLHQ 445
 419 LTRALDILVSLKSGELMDAYLHK 444

RESULT 5
 0920R9 PRELIMINARY; PRT; 444 AA.
 AC 0920R9;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE DELTA-6 FATTY ACID DESATURASE.
 GN FADS2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99085046; Pubmed=9867867;
 RA Cho H.-P., Nakamura M.T., Clarke S.D.;
 RT "Cloning, expression, and nutritional regulation of the mammalian
 RT delta-6 desaturase";
 RL J. Biol. Chem. 274:471-477(1999).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AF126798; AAD20017.1; -.
 DR HSSP; P00171; 1CYO.
 DR MGD; MGI:1930079; Fads2.
 DR InterPro; IPR001199; Cyt_B5.
 DR Pfam; PF00173; heme_1; 1.
 DR PRINTS; PR00363; CYTOCHROME_B5.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 444 AA; 52387 MW; 7615D17024D3B771 CRC64;

Query Match 64.3%; Score 1566.5; DB 11; Length 444;
 Best Local Similarity 62.8%; Pred. No. 3.5e-134;
 Matches 280; Conservative 62; Mismatches 101; Indels 3; Gaps 2;

QY	1	MGCVLRSPRREPRARQARVLPTFQWEOIYANDROQDKYLVTERRYUJDISYMAORNSR	60
Dd	1	MGKSGNOG--EGESTROARMPTFRMEIEIQKNLRTQMYLVIRKUYUTXKMSOHNRSGR	58
QY	61	LIDHNAEDQNTAFARFNODINLVYKJLOLLIGELARERERODRILMAOLVERPRLHO	120
Dd	59	VIGHNIGEDQNTAFARFNIDIRFGKYLKLYLIGELAREERYSIDKSSQUTERPRYLK	118
QY	121	AAEDMKLFDASTFFERALLGHIIMBEUAMLVLYLLGRQWESALAEPTLISAQOSMCL	180
Dd	119	TAEEDMVFNTNHLFFELLISHIYMESIAMFLLSYUGTOQMIRLTATLAVLTSORQAGYL	178
QY	181	QHLQJHASTIFKRSKMNHYAOKFVMSQCKGFSALWMPNRYAFONAKRPNFENDROPVAVR	240
Dd	179	QHDYGHLSYUUKSITNNVUHNKFEVGLKSGASAMWNNRYGONAKRPNFHNKDRPKSLNV	238
QY	241	FILGGE--SSEYQCKKRYKRLPRNOONIKFELTISPRLLTYNPEVELYAMLUQMOADLLV	299
Dd	239	FVLGEORPRLTYOKKAKLYRPNONHETRELLERGLRLRYMFOYQTLIMJISKRWJDLAM	298
QY	300	AAAFVAFPLSLRPRYGVUVLLFVAARVLRESNFWITQONNIPKDEIGNEKHNDWSS	359
Dd	299	ALSYUKRFYUUIPRYUGLIGLAVLANIRLESNHNFWUTQONNIMUEDIDNHRWFSS	358
QY	360	QLAATQNVPSLFTYMNFGSHLFOIEHNLPRRYRPNNTSRVARYLKSJCAKIGSYUWK	419
Dd	359	QLAATQNVQSFNMFNFGSHLFOIEHNLPRRYRPNNLKINARLYKSCAKHGEYQEK	418
QY	420	FLTALVDYLRSLKSGSDWIDAYUHQ	445
Dd	419	LRLALIDIVYLSLKSGLWIDAYUHK	444

RESULT	6
098SM7	
ID	098SM7
AC	098SM7
DT	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE	POTATIVE DELTA 6-DESATURASE.
GN	FD6D.
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC	Protactinopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX	NCBI_Taxid=8022;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=LIVER;
RA	Sellez I., Panseirat S., Kaushtik S., Bergot P.;
RT	"Cloning, tissue distribution and nutritional regulation of a delta-6-
RT	desaturase-like enzyme in rainbow trout.";
RL	Comp. Biochem. Physiol. B, Comp. Biochem. 130:83-93(2001).
CC	-1. SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC	EMBL: AF301910; AAK26745.1; -.
DR	HSSP; P00173; IAOA.
DR	InterPro: IPR001199; CYL_B5.
DR	Pfam: PF00173; heme_1; 1.
DR	PRINTS: PR00363; CYTOCHROMEB5.
DR	PROSITE: PS50255; CYTOCHROME_B5_2; 1.
DR	Heme.
SQ	SEQUENCE 454 AA; 52398 MM; 18E55D811420D537 CRC64;

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Query Match 57.9% Score 1410 DB 13 Length 454;
Best Local Similarity 58.6% Pred. No. 6.2e-120;
Matches 260; Conservative 56; Mismatches 120; Indels 8; Gaps 2.

      3 GVEPGEPRGPAQGFALFECMEQIRAHDDGDKWLYERRVYDISRMARHPGGSRLI 62
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      18 GVPDPGGRGSA-----VYMEWEQKGRCHRSKRWLIDKRVYNIQMAKRHPGGVRI 70
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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[illegible]

RESULT	7	
Q90ZEH		
ID	Q90ZEH	PRELIMINARY; PRT: 454 AA.
AC	Q90ZEH;	
DT	01-DEC-2001 (TREMBLrel. 19, Created)	
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE	PUTATIVE DELTA 6-DESATURASE.	
GN	pp6d.	
OS	Oncorhynchus masou (Cherry salmon) (Masu salmon)	
OC	Actinoptera; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;	
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.	
OC	NCBI_TaxId=8020;	
OR	[1]	
RA	SEQUENCE FROM N.A.	
RA	YOSHIZAKI G., ISHIKAWA A., TAKEUCHI T., GEN K.;	
RT	"delta6-desaturase-like cDNA in masu salmon.";	
RL	Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.	
Q0	EMBL: AB070444; BAB63440.1; -	
Q0	SEQUENCE 454 AA; 52480 MW; 9FA556A7AECCF76 CRC64;	

[illegible]


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DB 351 LGDQPPVBYGKIKLKIPIYHOFELVGPRLIPVFFNLIQIRYFESQBDVADLAWM 310
QY 302 SFYAFELSLPEYGVPGVLLFEVAVRYLESHEWVITOMNHPIKEIGHEKRDWVSOL 361
DB 311 TFLYRFCCYPPFFGFGVALISFVRFLSHWFWYTOHSHLPMENDHRODMITMOL 370
QY 362 AATCNVPSLETWNFSGHINFOIENHLPFRMRNRYSVAVLYSKCAKGLSTYEVKPL 421
DB 371 SATCNIGSTFNDWFGSHINFOIENHLPFRMRNRYSVAVLYSKCAKGLSTYEVKPL 430
QY 422 TALVDIVRSLSKSGDIWLDAYLHQ 445
DB 431 KGMTDVVRSLSKSGDIWLDAYLHK 454

RESULT 8
Q9H3G3 PRELIMINARY: PRT: 422 AA.
ID Q9H3G3
AC Q9H3G3
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE F5327.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=MESOTHELIAL;
RA Zhang J.S., Reddel R.R.;
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF108658; AAC63192.1;
SQ SEQUENCE 422 AA; 49326 MW; AA47EB76FB1FFA4 CRC64;

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Query Match 56.58; Score 1376.5; DB 4; Length 422;
Best Local Similarity 62.88; Pred. No. 6.3e-117;
Matches 246; Conservative 49; Mismatches 92; Indels 5; Gaps 2;

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DB 55 HGGGRLIGHGADATDAPAFRPHODLNFRKFLQPLILGELAPERSODPLNAQVLED 114
QY 35 HNASM----GHRITGGQDAPAFRPHODLNFRKFLQPLILGELAPERSODPLNAQVLED 90
DB 115 FALAKKTEEDMNLFRKTHVFFLLLAHITALESTAMFVYFFGNGMIPTLITAFVATSO 150
QY 175 AOSWCLQDHLGASIFKKSMMNNHVAOKFVWGOLKGSASAMWNRFRFOHNAKPIEFKDP 234
DB 151 AONAGLQDHYGLHLSYVRKPKRNHLVYKFIYGLHKGASAMWNNHFRFOHNAKPIEFKDP 210
QY 235 VYVAVPEVLGE--SSVEYGGKKRRRLPYNOOHLYFELIGPRLTLVNEVEMLAMLYCMQ 293
DB 211 VMKLAVFVEMQDIEYGGKKRLPYNOOHLYFELIGPRLTLVNEVEMLAMLYCMQ 270
QY 294 MADLMAASFARFELSLPEYGVPGVLLFEVAVRYLESHEWVITOMNHPIKEIGHEK 353
DB 271 WYDLMAVSYIRFETIYIPFYGLGALLFNIRFLSHWFWYTOHSHLPMENDHRODMITMOL 330
QY 354 RQWVSQALATCNVPSLETWNFSGHINFOIENHLPFRMRNRYSVAVLYSKCAKGL 413
DB 331 RQWVSQALATCNVPSLETWNFSGHINFOIENHLPFRMRNRYSVAVLYSKCAKGL 390
QY 414 SYEVRPFLTALVDIVRSLSKSGDIWLDAYLHQ 445
DB 391 EYQERPLRALDIIRLSKSGKIMLDAYLHK 422

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RESULT 9
Q9DEX7 PRELIMINARY: PRT: 444 AA.
ID Q9DEX7

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AC Q9DEX7;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PUTATIVE DELTA-6 FATTY ACYL DESATURASE.
GN FADS6.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Hastings N., Agaba M.K., Tocher D.R., Teale A.J., Sargent J.R.;
RT "The Evolution of Delta-6 Fatty Acyl Desaturase Genes in Marine and
RT Freshwater Teleosts."
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: AF309556; AAC25710.1;
DR HSSP: P00173; 1A0A.
DR InterPro: IPR001199; Cyt-B5.
DR Pfam: PF00173; Heme_1; 1.
DR PRINTS: PR00363; CYTOCHROME_B5.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KM Heme.
SQ SEQUENCE 444 AA; 52032 MW; 6AA25A1DC1DC0F65 CRC64;

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Query Match 55.88; Score 1359.5; DB 13; Length 444;
Best Local Similarity 54.38; Pred. No. 2.4e-115;
Matches 243; Conservative 72; Mismatches 128; Indels 3; Gaps 2;

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DB 1 MGGGQGGQIDR--ITDQNRSSSYTMEVQKTKGQWVYVRYKYYNVSQVKKHNGGLR 58
QY 61 LGHHCAGATDAPAFRPHODLNFRKFLQPLILGELAPERSODPLNAQVLED 120
DB 59 IIGHVAGDEALFAFAPRNQDLVRYKLYKPLILGELASEPSODRQKNAALVEDEFLRE 118
QY 121 AEDMKLFDPASPTFFAFGLIHLAMEVLAHLIYLLGPGVPSALAPFLAISQAQSWCL 180
DB 119 RLEAGCFTQPLRLALHSHIILLLEALFAMVWYVGTGQWITLIVAVIATPAGSQGWL 178
QY 181 QHDLGASIFKKSMMNNHVAOKFVWGOLKGSASAMWNRFRFOHNAKPIEFKDP 240
DB 179 QHDFGLSVFSGKNNHLVYKFIYGLHKGASAGAMWNNHFRFOHNAKPIEFKDP 238
QY 241 FLLGE--SSVEYGGKKRRRLPYNOOHLYFELIGPRLTLVNEVEMLAMLYCMQ 299
DB 239 FVVGQNPVPEYGVKIKLIRYNOHKKYFFIGPRLIPYFOGFLNNHISHGMVYDLW 298
QY 300 AASFYARFELSLPEYGVPGVLLFEVAVRYLESHEWVITOMNHPIKEIGHEKRDWVS 359
DB 299 CISTYVRFLCTQYGYFMAIILFNFRWESHMWYTOHSHLPMENDHRODMITMOL 358
QY 360 QLATCNVPSLETWNFSGHINFOIENHLPFRMRNRYSVAVLYSKCAKGLSTYEVK 419
DB 359 QLATCNVPSLETWNFSGHINFOIENHLPFRMRNRYSVAVLYSKCAKGLSTYEVK 418
QY 420 FLTALVDIVRSLSKSGDIWLDAYLHQ 445
DB 419 LYGAADITRSLKSGELMDAYLHK 444

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RESULT 10
ID 060426 PRELIMINARY: PRT: 352 AA.
AC 060426;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

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DE BC69730.1 (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RA SEQUENCE FROM N.A.
 RP Lameddin J.E., McCready P.M., Coleman M., Skowronski E., Adamson A.W.,
 RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
 RA Dangnan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
 RA Liu S., Attix C., Andreise T., Tranheim M., Amico-Keller G.,
 RA Coeffield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
 RA Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
 RA Kodayashii A., Olsen A.S., Carrano A.V.,
 RT "Sequence analysis of a human BAC containing the FEN1 DNA repair
 gene.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC004770; AAC23396.1; -.
 FT NON_TER
 SQ SEQUENCE 352 AA; 39851 MW; 488341D5A1672399 CRC64;

Query Match 54.9%; Score 1338.5; DB 4; Length 352;
 Best Local Similarity 81.2%; Pred. No. 1.4e-113;
 Matches 204; Conservative 6; Mismatches 26; Indels 29; Gaps 5;
 QY 72 DAFAFHODLNFVRKFLQPLLIGELAPESQDGPLNAQLVEDFRALHQAEDMKLFQAS 131
 DB 1 DAFAFHODLNFVRKFLQPLLIGELAPESQDGPLNAQLVEDFRALHQAEDMKLFQAS 60
 QY 132 PTFEAFLLGIIAMEVLALYLILGPGWVSALAFLIALISOAGSMCLOHDIHSHATK 191
 DB 61 PTFEAFLLGIIAMEVLALYLILGPGWVSALAFLIALISOAGSMCLOHDIHSHATK 120
 QY 192 KSMWNVAQKFWGOLKGSAMWNRFRFOHAKPNIFKDPDYVAPVPLIGESSVEG 251
 DB 121 KSMWNVAQKFWGOLKGSAMWNRFRFOHAKPNIFKDPDYVAPVPLIGESSVEG 180
 QY 252 KKKRRRLPYNOOHLFFELIGPRLTLVFEVENLAVMLVCOMADLLMAAFYAREFLSY 311
 DB 181 KKKRRRLPYNOOHLFFELIGPRLTLVFEVENLAVMLVCOMADLLMAAFYAREFLSY 240
 QY 312 LPFYGVGVLLFFVAVRVLESHEFWITQNMHI--PKFIEGHEKRPWVSQSLAATCNVVP 369
 DB 241 LPFYGVGVLLFFVAVRVLESHEFWITQNMHI--PKFIEGHEKRPWVSQSLAATCNVVP 283
 QY 370 SFTTNFSGHLPFOIENHLPFMRPR 394
 DB 284 -----RGALTF--HQLVQRAPO 298

RESULT 11
 Q96H07 PRELIMINARY; PRT; 386 AA.
 AC Q96H07;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE PRTY ACID DESATURASE 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RA SEQUENCE FROM N.A.
 RP TISSUE-BRAIN, AND ANAPLASTIC OLIGODENDROGLIOMA WITH 1P/19Q LOSS;
 RA Strausberg R.;
 RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC009011; AAH09011.1; -.
 SQ SEQUENCE 386 AA; 45524 MW; 2A187A9CBFFEF32 CRC64;

Query Match 54.5%; Score 1328.5; DB 4; Length 386;
 Best Local Similarity 61.0%; Pred. No. 1.3e-112;
 Matches 236; Conservative 55; Mismatches 93; Indels 3; Gaps 2;
 QY 1 MGVGEPRREGPAQPGAPLPFCWEIOIRAHODPGDKMLVIERRYDISRWAKRPGGR 60
 DB 1 MGVGEPRREGPAQPGAPLPFCWEIOIRAHODPGDKMLVIERRYDISRWAKRPGGR 58
 QY 61 LIGHGADATDARAFHODLNFVRKFLQPLLIGELAPESQDGPLNAQLVEDFRALHQA 120
 DB 59 VIGHGADATDARAFHODLNFVRKFLQPLLIGELAPESQDGHKNSKTDEFRALHQA 118
 QY 121 AAEEMKLPDASPFEPFALLGIIAMEVLALYLILGPGWVSALAFLIALISOAGSMC 180
 DB 119 TAEEDMKLPDASPFEPFALLGIIAMEVLALYLILGPGWVSALAFLIALISOAGSMC 178
 QY 181 OHDLGHSIFKRSWNNHVAQKFWGOLKGSAMWNRFRFOHAKPNIFKDPDYVAPV 240
 DB 179 OHDLGHSIFKRSWNNHVAQKFWGOLKGSAMWNRFRFOHAKPNIFKDPDYVAPV 238
 QY 241 FLIGE-SSVEYGGKRRRYLPYNOOHLFFVAVRVLESHEFWITQNMHI--PKFIEG 299
 DB 239 FLIGEMQPIEXGKKKKLXLPYNNHHEFFLIGPRLTLVFEVENLAVMLVCOMADLLM 298
 QY 300 AASFARFELSYLPFGVGVLLFFVAVRVLESHEFWITQNMHI--PKFIEGHEKRPWVS 359
 DB 299 AASYIRFFITYIPFYGIIIGALLNFIFLESHEFWITQNMHI--PKFIEGHEKRPWVS 358
 QY 360 QLAATCNVPSLFTNMFSGHLPFOIENH 386
 DB 359 QLAATCNVPSLFTNMFSGHLPFOIENH 385

RESULT 12
 Q9DEX6 PRELIMINARY; PRT; 444 AA.
 AC Q9DEX6;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE PUTATIVE DELTA-6 FATTY ACYL DESATURASE.
 GN FADS6.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes;
 OC Cypriniformes; Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RA SEQUENCE FROM N.A.
 RP Hastings N., Agaba M.K., Tocher D.R., Teale A.J., Sargent J.R.;
 RT "The Evolution of Delta-6 Fatty Acyl Desaturase Genes in Marine and
 RT Freshwater Teleosts."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -I SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AF309557; AAC25711.1; -.
 DR HSSP; P00171; ICYO.
 DR InterPro: IPR001199; CYL_B5.
 DR Pfam: PF00173; heme_1; 1
 DR PRINTS; PR00363; CYTOCHROME_B5.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 444 AA; 51963 MW; 6EDA2A51AB091A7 CRC64;

Query Match 54.4%; Score 1326.5; DB 13; Length 444;
 Best Local Similarity 53.8%; Pred. No. 2.4e-112;
 Matches 240; Conservative 71; Mismatches 132; Indels 3; Gaps 2;
 QY 1 MGVGEPRREGPAQPGAPLPFCWEIOIRAHODPGDKMLVIERRYDISRWAKRPGGR 60
 DB 1 MGVGEPRREGPAQPGAPLPFCWEIOIRAHODPGDKMLVIERRYDISRWAKRPGGR 58
 QY 61 LIGHGADATDARAFHODLNFVRKFLQPLLIGELAPESQDGPLNAQLVEDFRALHQA 120

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: October 7, 2002, 11:38:26 ; Search time 15.96 Seconds
(without alignments)
681.039 Million cell updates/sec

Title: US-09-806-088-3

Perfect score: 2437
Sequence: 1 MCGVGPGRBPPAQCAGL.....DIVRSLSKSGDIDWATYHQ 445

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total: number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCUTS.COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	650	26.7	143	2	US-08-834-655-11
2	650	26.7	143	3	US-08-834-033A-12
3	650	26.7	143	4	US-08-834-574-11
4	478.5	19.6	457	2	US-08-834-655-2
5	478.5	19.6	457	3	US-08-834-033A-2
6	478.5	19.6	457	4	US-09-363-574-2
7	477.5	19.6	457	2	US-08-834-610-4
8	477.5	19.6	457	3	US-08-834-033A-14
9	471	19.3	131	2	US-08-834-655-9
10	471	19.3	131	3	US-08-834-033A-10
11	471	19.3	131	4	US-09-363-574-9
12	438	18.0	452	4	US-08-934-254-27
13	432	17.3	448	1	US-08-366-779-5
14	432	17.3	448	1	US-08-789-936-5
15	432	17.3	448	1	US-08-834-254-5
16	420	17.2	446	2	US-08-833-610-5
17	420	17.2	446	2	US-08-834-033A-15
18	392.5	16.1	355	2	US-08-834-655-5
19	392.5	16.1	355	3	US-08-834-033A-6
20	392.5	16.1	355	4	US-09-363-574-5
21	311.5	12.8	446	2	US-08-833-610-2
22	311.5	12.8	446	3	US-08-834-033A-5
23	236	9.7	365	2	US-08-833-610-7
24	236	9.7	365	3	US-08-834-033A-17
25	217.5	8.9	252	2	US-08-834-655-7
26	217.5	8.9	252	3	US-08-834-033A-8
27	217.5	8.9	252	4	US-09-363-574-7

28	210	8.6	359	1	US-08-307-382-2	Sequence 2, Appl
29	210	8.6	359	1	US-08-366-779-2	Sequence 2, Appl
30	210	8.6	359	1	US-08-478-727-2	Sequence 2, Appl
31	210	8.6	359	1	US-08-473-508-2	Sequence 2, Appl
32	210	8.6	359	1	US-08-789-936-2	Sequence 2, Appl
33	210	8.6	359	2	US-08-833-610-6	Sequence 6, Appl
34	210	8.6	359	3	US-08-834-033A-16	Sequence 16, Appl
35	210	8.6	359	4	US-08-934-254-2	Sequence 2, Appl
36	161.5	6.6	399	2	US-08-834-655-4	Sequence 4, Appl
37	161.5	6.6	399	3	US-08-834-033A-4	Sequence 4, Appl
38	161.5	6.6	399	4	US-09-363-574-4	Sequence 4, Appl
39	153	6.3	87	2	US-08-834-655-10	Sequence 10, Appl
40	153	6.3	87	3	US-08-834-033A-11	Sequence 11, Appl
41	153	6.3	87	4	US-09-363-574-10	Sequence 10, Appl
42	148.5	6.1	424	4	US-09-161-994A-4	Sequence 4, Appl
43	147.5	6.1	386	4	US-08-244-205-2	Sequence 2, Appl
44	147.5	6.1	386	4	US-09-161-994A-11	Sequence 11, Appl
45	147.5	6.1	386	5	PCT-US92-10284-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-834-655-11
; Sequence 11, Application US/08834655
; Patent No. 5968809
GENERAL INFORMATION:
APPLICANT: KUTZON, DEBORAH
APPLICANT: MURKERT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSER: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 143 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-11

Query Match 26.7%; Score 650; DB 2; Length 143;
Best Local Similarity 87.2%; Pred. No. 8.2e-63;
Matches 110; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 285 LAYMLVCMQADLLMAASFARFSLYLPFYGVGVLLFFVAVRVLESHPFWITOMNHI 344
 DB 11 LAYMLVCMQADLLMAASFARFSLYLPFYGVGVLLFFVAVRVLESHPFWITOMNHI 70
 QY 345 PREIGHEKRDWVSSQLATCNVPSLFTNMFSGHLNFOIEHNLPRPRHNSRVAPLV 404
 DB 71 PREIGHEKRDWVSSQLATCNVPSLFTNMFSGHLNFOIEHNLPRPRHNSRVAPLV 130
 QY 405 KSLCAKHGLSYEV 417
 DB 131 KAFCAKHGLHYEV 143

RESULT 2
 US-08-834-033A-12
 ; Sequence 12, Application US/08834033A
 ; Patent No. 6075183
 ; GENERAL INFORMATION:
 ; APPLICANT: KNUITZON, DEBORAH
 ; APPLICANT: MUKERJI, PRADIP
 ; APPLICANT: HUANG, YUNG-SHENG
 ; APPLICANT: THURMOND, JENNIFER
 ; APPLICANT: CHAUDHARY, SUNITA
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
 ; STREET: 2001 FERRY BUILDING
 ; CITY: SAN FRANCISCO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/834,033A
 ; FILING DATE: 11-APR-1997
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WARD, MICHAEL R.
 ; REGISTRATION NUMBER: 38,651
 ; REFERENCE/DOCKET NUMBER: CGAB-300, USA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 433-4150
 ; TELEFAX: (415) 433-8716
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 143 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-834-033A-12

Query Match 26.7%; Score 650; DB 3; Length 143;
 Best local Similarity 87.2%; Pred. No. 8, 2e-63;
 Matches 116; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 285 LAYMLVCMQADLLMAASFARFSLYLPFYGVGVLLFFVAVRVLESHPFWITOMNHI 344
 DB 11 LAYMLVCMQADLLMAASFARFSLYLPFYGVGVLLFFVAVRVLESHPFWITOMNHI 70
 QY 345 PREIGHEKRDWVSSQLATCNVPSLFTNMFSGHLNFOIEHNLPRPRHNSRVAPLV 404
 DB 71 PREIGHEKRDWVSSQLATCNVPSLFTNMFSGHLNFOIEHNLPRPRHNSRVAPLV 130

QY 405 KSLCAKHGLSYEV 417
 DB 131 KAFCAKHGLHYEV 143

RESULT 3
 US-09-363-574-11
 ; Sequence 11, Application US/09363574
 ; Patent No. 6136574
 ; GENERAL INFORMATION:
 ; APPLICANT: KNUITZON, DEBORAH
 ; APPLICANT: MUKERJI, PRADIP
 ; APPLICANT: HUANG, YUNG-SHENG
 ; APPLICANT: THURMOND, JENNIFER
 ; APPLICANT: CHAUDHARY, SUNITA
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
 ; STREET: 2001 FERRY BUILDING
 ; CITY: SAN FRANCISCO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/363,574
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WARD, MICHAEL R.
 ; REGISTRATION NUMBER: 38,651
 ; REFERENCE/DOCKET NUMBER: CGAB-202, USA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 433-4150
 ; TELEFAX: (415) 433-8716
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 143 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-363-574-11

Query Match 26.7%; Score 650; DB 4; Length 143;
 Best local Similarity 87.2%; Pred. No. 8, 2e-63;
 Matches 116; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 285 LAYMLVCMQADLLMAASFARFSLYLPFYGVGVLLFFVAVRVLESHPFWITOMNHI 344
 DB 11 LAYMLVCMQADLLMAASFARFSLYLPFYGVGVLLFFVAVRVLESHPFWITOMNHI 70
 QY 345 PREIGHEKRDWVSSQLATCNVPSLFTNMFSGHLNFOIEHNLPRPRHNSRVAPLV 404
 DB 71 PREIGHEKRDWVSSQLATCNVPSLFTNMFSGHLNFOIEHNLPRPRHNSRVAPLV 130
 QY 405 KSLCAKHGLSYEV 417
 DB 131 KAFCAKHGLHYEV 143

RESULT 4
 US-08-834-655-2
 ; Sequence 2, Application US/08834655
 ; Patent No. 5968609

GENERAL INFORMATION:

APPLICANT: KUTZON, DEBORAH
 APPLICANT: MURKERT, PRADIP
 APPLICANT: HUANG, YONG-SHENG
 APPLICANT: THURMOND, JENNIFER
 APPLICANT: CHAUDHARY, SONITA
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RAE-VENTER LAM GROUP, P.C.
 STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
 CITY: PALO ALTO
 STATE: CA
 COUNTRY: USA
 ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/834,655
 FILING DATE: 11-APR-1997
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: RAE-VENTER, BARBARA
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: CGNE.124.000S
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 328-4400
 TELEFAX: (650) 328-4477
 TELEX: N/A

INFORMATION FOR SEQ. ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 457 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-834-655-2

Query Match 19.6% Score 478.5; DB 2; Length 457;

Best Local Similarity 26.7% Pred. No. 2,1e-43;

Matches 117; Conservative 86; Mismatches 165; Indels 71; Gaps 16;

39 LVIERRYDISRMAQRHGGSLRGHGAEDATDAFRAFHODLNFVRKFTLOPLIGELAP 98
 34 MIDNKYVDAREFVDPHGGSVILTHVG-KDGDVDFTFHPEAM--ETLANFVGD1-- 88
 99 EEPSSDGPLNQLVEDFRALHQAEDMKLFDAFPEFAFLGHIILAMEVLMLIYLGP 158
 89 DESDSD-1KNDPFAEVRKLTFLFOSLGYDSSKAYAFKVSFNLCT---WGLSTVIYA 143
 139 GW-----VPSLAAPFLIALISQASQWGLDLDLGHASIFKSKSMNNHYAOKFVWGLKGSFSAH 213
 144 KMGQSTLANVLSALGLDFWQCGWLADFLHGOVFDREWGDLFGAFLGVCQGGSSS 203
 214 WNNFRHFOHAKPNIFKHPDVTVAFVLLGESSV-----EYGRKKRRYLPYNOQH 264
 204 WNKDKHNTNHAAPRVHGGEDPDITNPLITWSEHALEMESDVPDELTFRMSRFVNLQTM 263
 265 LFFLPGPLTLTVNE--VENLAYML-----VCQMADLLNA 300
 264 FYF-----PILSPARKLSMCLQSLIFLPRNGQAKRSGARVPISLVEQLSLAMWT---W- 314
 301 ASFAARFLSLTPYGV-GLVLEFYAVVLESHMFVITQMNH-----IPKEIGEKHR 354
 315 --YLATMEL---FKDPVNLVYFLVSQVGNLLAVFSLNHNKMPVYSKE--EAYDM 366
 355 DWVSQSLAATCNVPSLFTNMFSGLHLPQIEHHLFPRMRHNYSRVAPLVKSLCAKHGLS 414

DB 367 DFFTKOITGSDVHPGLFANMFTGILNQIEHHLFPRMRHNSKIOAPAVETLCKRYNR 426

QY 415 YEVRPEFLAVDIYRSLK 433

DB 427 YHTGMTEGTAEVPSRLNE 445

RESULT 5

US-08-834-033A-2

; Sequence 2, Application US/08834033A

; Patent No. 6075183

; GENERAL INFORMATION:

; APPLICANT: KUTZON, DEBORAH

; APPLICANT: MURKERT, PRADIP

; APPLICANT: HUANG, YONG-SHENG

; APPLICANT: THURMOND, JENNIFER

; APPLICANT: CHAUDHARY, SONITA

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.

; STREET: 2001 FERRY BUILDING

; CITY: SAN FRANCISCO

; STATE: CA

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/834,033A

; FILING DATE: 11-APR-1997

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: WARD, MICHAEL R.

; REGISTRATION NUMBER: 38,651

; REFERENCE/DOCKET NUMBER: CGAB-300. USA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 433-4150

; TELEFAX: (415) 433-8716

; TELEX: N/A

; INFORMATION FOR SEQ. ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 457 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-834-033A-2

Query Match 19.6% Score 478.5; DB 3; Length 457;

Best Local Similarity 26.7% Pred. No. 2,1e-43;

Matches 117; Conservative 86; Mismatches 165; Indels 71; Gaps 16;

39 LVIERRYDISRMAQRHGGSLRGHGAEDATDAFRAFHODLNFVRKFTLOPLIGELAP 98
 34 MIDNKYVDAREFVDPHGGSVILTHVG-KDGDVDFTFHPEAM--ETLANFVGD1-- 88
 99 EEPSSDGPLNQLVEDFRALHQAEDMKLFDAFPEFAFLGHIILAMEVLMLIYLGP 158
 89 DESDSD-1KNDPFAEVRKLTFLFOSLGYDSSKAYAFKVSFNLCT---WGLSTVIYA 143
 139 GW-----VPSLAAPFLIALISQASQWGLDLDLGHASIFKSKSMNNHYAOKFVWGLKGSFSAH 213
 144 KMGQSTLANVLSALGLDFWQCGWLADFLHGOVFDREWGDLFGAFLGVCQGGSSS 203
 214 WNNFRHFOHAKPNIFKHPDVTVAFVLLGESSV-----EYGRKKRRYLPYNOQH 264
 204 WNKDKHNTNHAAPRVHGGEDPDITNPLITWSEHALEMESDVPDELTFRMSRFVNLQTM 263

Page 4

QY	99	EPESODGELAAQVLEDFRRLHQAEDKJLEBAPREFFALGHIAEVLAMLTLLGLP	158
Dd	89	DSDARD-1KNDPBAEVRKRLPTLFQSLGYDSSKAYAFKVSFNLCT----	WGLSTVYA 143
QY	159	GM-----VPSLAAFLAITSANOCSMCOHDLGASIFKSKMNNVNOAKPYMOQLGSPAH	213
Dd	144	KKGOTSTLANVLSALLGSLTMOQSGMLHNDPHHOVFDQREMDLFGALFAGGCGGSESS	203
QY	214	WNNFRHOHNAKPNIEHKKDPDYAVARVELLGESSV-----EYKKKKRYRLPYNOH	264
Dd	204	WKKDKNNHNAALVNVGDEPDDIHNPLRTTWSHALEMESDVPDEELRBMRSRPVYLNQTW	263
QY	265	LYEFLIGRPILLTYNDE--VENILATML-----VCQOMADLLMA	300
Dd	264	RYF-----PLTSARLSMCLQSLFYLVRNOAQRBSGARVPLSLVEQSLAMNMT--W-	314
QY	301	ASPYARFPLSLTPRYVP--GULLFPGVAVRVLSHMFVWITOMNH-----IPKEIGHEKRR	354
Dd	315	--YLATMLFL-----FINDRPNNMLUYFLVSOAGNMLATYFSLTINNGRPVYSK--EAYDM	366
QY	355	DWSSQLATCONPESLPTFNPSGHLENOLEHLEPRPNNYRSYAVRLPYLVSCKAHOLS	414
Dd	367	DEFTQIITIGDHYNGPGLFANMETGSLVNOLEHLEPRSPMRHNEFKIQPAVELTCKKYNVR	420
QY	415	YEVKRFELALVDIYRSKX	433
Dd	427	YHTTGMIEGTAEVFSRLNE	445

RESULT 7
 US-08-833-610-4
 Sequence 4, Application US/0883610
 Patent No. 5972664
 GENERAL INFORMATION:
 APPLICANT: KNUTZON, DEBORAH
 APPLICANT: MURRELLI, PRADIP
 APPLICANT: HUANG, YONG-SHENG
 APPLICANT: THORNDYK, JENNIFER
 APPLICANT: CHAUDHARY, SUNTA
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 STREET: 260 SHERIDAN AVE, P.O. BOX 60039
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/833,610
 FILING DATE: 11-APR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: RAE-VENTER, BARBARA
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: CGNE.123.000US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)328-4400
 TELEFAX: (650)328-4477
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 457 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

Tue Oct 8 10:29:15 2002

us-09-806-088-3.rai

Page 6

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1 COMPUTER: IBM PC compatible
2 OPERATING SYSTEM: PC-DOS/MS-DOS
3 SOFTWARE: PatentIn Release #1.0, Version #1.30
4 CURRENT APPLICATION DATA:
5 APPLICATION NUMBER: US/08/834,655
6 FILING DATE: 11-APR-1997
7 CLASSIFICATION: 435
8 ATTORNEY/AGENT INFORMATION:
9 NAME: RAE-VENTER, BARBARA
10 REGISTRATION NUMBER: 32,750
11 REFERENCE/DOCKET NUMBER: CGWE.124.00US
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: (650) 328-4400
14 TELEFAX: (650) 328-4477
15 TELEX: N/A
16 INFORMATION FOR SEQ. ID NO.: 9:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 131 amino acids
19 TYPE: amino acid
20 STRANDEDNESS: not relevant
21 TOPOLOGY: linear
22 MOLECULE TYPE: peptide
23 US-08-834-655-9

```

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Query Match      19.3% Score 471: DB 2: Length 131:
Best Local Similarity 65.9%: pred. No. 2e-43:
Matches 81: Conservative 14: Mismatches 28: Indels 0: Gaps 0:

OY 297 LLMASAFYAFNFFLSYLPFYGVPGVLLFFPAVAVLESHNMFVITQNHAIPEKIGHGKRDW 356
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 LAMNITTYVAFPELLYVPLGLGKAFGLFLPTVAFLESHNMFVWVITQNHIIPHIIDRRMDW 67

OY 357 VSSOLAATCNVERESGLTFNMFSGHLNQIDHILFPKPRPNRNTSRAPLYKSLCAKHGILSYE 416
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 VSTOLAATCNVHKSAFNDFWFSGLHFNQIDHILFPPMPRNHXYAPLVQSLCAKHGILEYQ 127

OY 417 VKP 419
      | |
Db 128 SKP 130

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RESULT 10
US-08-834-033A-10
Sequence 10, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KNOTZON, DEBORAH
APPLICANT: KUREKJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 PERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834, 033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.

```

?      REGISTRATION NUMBER:   38,651
?      REFERENCE/DOCKET NUMBER: CGAB-300.USA
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE:    (415) 433-4150
?      TELEFAX:     (415) 433-8716
?      TELEX:       N/A
?      INFORMATION FOR SEQ ID NO: 10:
?      SEQUENCE CHARACTERISTICS:
?          LENGTH: 131 amino acids
?          TYPE: amino acid
?          STRANDEDNESS: not relevant
?          TOPOLOGY: linear
?      MOLECULE TYPE: peptide
US-08-834-033A-10

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[illegible]

RESULT 11
US-09-363-574-9
Sequence 9, Application US/09363574
Patent No. 6136574
GENERAL INFORMATION:
APPLICANT: KNOTZON, DEBORAH
APPLICANT: MOKERUTJ, FRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUDITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids

TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-574-9

Query Match 19.3%; Score 471; DB 4; Length 131;
Best Local Similarity 65.9%; Pred. No. 2e-43;
Matches 81; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

QY 297 LLMASFYARFELSYLPEYGVPLLFYAVVLSHMFVWITQNHLPKEIGHEKRDW 356
DB 8 LAMITEYVREPLLYVPLGLKAFGLFTVFELESNFWVWQNHIMHIDHRNDW 67
QY 357 VSSOLATCNVDESLFTNWFSGHLNFOIEHHLPFRPHNYSRAVPLKSLCAKHGLSYE 416
DB 68 VSTOLATCNVHSANFNDWFSGHLNFOIEHHLPFRPHNYSRAVPLVQSLCAKHGLIETQ 127
QY 417 VKP 419
DB 128 SKP 130

RESULT 12

US-08-934-254-27
Sequence 27 Application US/08934254
Patent No. 6335861

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83832YXWV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR

INFORMATION FOR SEQ. ID NO: 27:

SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-934-254-27

Query Match 18.0%; Score 438; DB 4; Length 452;
Best Local Similarity 28.4%; Pred. No. 5.1e-39;
Matches 129; Conservative 64; Mismatches 172; Indels 90; Gaps 18;

QY 26 EDIRAHDPGRKWLVIERRVYDISRMAQRPGSRLIGHGADATDAFRAHODLNFVR 85
DB 12 EDIRRHNSGDLWISIDQKVDYDCSRMAEHRGGEVPLLSLAGODVDTADIAVHPGTAW-- 69

QY 86 KLEPPLIG--ELAPEPSODGPLNQLVEDTRALHQAEDMKLPDASPTFEAFILGH-- 141
DB 70 RHLDPLFTGYVYLKDEFS-----EISKDYRLINEMSSSGIFEK-----GHAI 114
QY 142 ---ILAMEVILMLIY-----LLPGVWPSLAFAILAIISQASWICLQR 182
DB 115 MMTFVGAVVMAALIVGVLASSESVGHMLGALLGLMLNQAAYG-----H 160
QY 183 DLGHASIFKSSWNHNAQAKVGMQLGFSASAMWNRHGHAKRPIFKPDYVAVPEL 242
DB 161 DSGHYQVMPTRGNRITQLAGNLTGISIAWKKTHNHLACSDLDYDDLOHIVFA 220
QY 243 LGE-----SSVEYK-----KKRRLPYNOOHLVFFLIGPPLTL--VNFVEVNLAYML 289
DB 221 VSTRPLNITSVFGRVLKFEDEVARFLVSYQHWYV-----PVMIFGRVNLFIOTPLLL 275
QY 290 VCMQAD-----LLMASFYARF--FLSYLPEYGV--GVLLFVAVVLSHMFVWITO 340
DB 276 TRDVPDRALNMGIAVFWIWFPLEVSCLPNW--PERGFLVLSRAVYAIQHOFT----- 329
QY 341 MNHLPKE--IGHEKRDWSSOLAATCNVEPSLFTNWFSGHLNFOIEHHLPFRPHNYS 388
DB 330 LNHFSGDTYVGPCKDWNFEKQTKGTIDITCPMDWDFGGLOFQLEHHLPRLRGOLR 389
QY 399 RVAPLVKSLCAKHGLSYEVKPFLLTALVDIVRSLK 432
DB 390 KIAPLARDLCKKHGMFPRSGFMDANVHTIRTLR 424

RESULT 13

US-08-366-779-5
Sequence 5 Application US/08366779
Patent No. 5614393

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,779
FILING DATE: 30-DEC-1994
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83832YXW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR

INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-366-779-5

Query Match	17.3%;	Score 422;	DB 1;	Length 448;
Best Local Similarity	26.8%;	Pred. No. 2.8e-37;		
Matches 120;	Conservative 72;	Mismatches 182;	Indels 74;	Gaps 15;

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OY      26 EOIIRADQGDWMLTIERRYVDIERNQAORPGSRLLIGHGAEADNTDAFRPHO-----79
       :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      12 DEKNDKRKGDMITIGOKAIDVADWDKRDPRGSFPLKSAGOEYTDFAVAFHASTWKXN 71
OY      80 -DINPVRKFLDPRLIGELAPRPSODGRPLNAQLVEDFRALHOAADMKLFASPTFEFATL 138
Db      72 LDFFFTGYLAKDYSEVS-----KYRIKLVPEFSKMJLYDK-----109
OY      139 LGHTL-----ADEVTAMLLIY--LLGGWPSPALAAFIILAQASWCLOJDHGHSIFK 191
       ||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      110 -GHMTRATLCETAMLFPANSTGVGLFCGVLVHLFSCLMGELMTOSGIMGADCHAWVVS 168
OY      192 KSMNNPVAOKFVMQOLGFSAMWNFRFHONAHKPIFKRDDVTVAVPFLTG-----244
Db      169 DSRLEKFMGIFFANCLSGISIGMKKNHNHAIACSLSDYDDLDGIYFLVSSKFEGSL 228
OY      245 -----ESSVEYKKKKRRKLRFNOQHLLFELLGPLL-PLVNFEEVENTAYML-----YCMQ 293
Db      229 TSHFYERKRTLFESLSREFVSY--OHMFYU---PICCAARLMKYVOISLIMTLIKRNYSYR 282
OY      294 MADLLMAA--SEYARFFESTYRFGYGVLVLFVFA---VRLESHPFWAITOMNHIPKE- 347
       ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      283 AOLLILOCLVFSTWYLVLAVSCLRPMNGER--TMFVIAIASLTGMOOVQF-----SLMHSSSV 336
OY      348 -IGHEKHNDWASSQLAATCNVERPSLFTNWFSGLNFQIEHNLFRPMRPANTRYAVPLVKS 406
Db      337 YVGKRGKGNMEKORDGTDLIDISCPRMDWDFNGSSQFOEHNHLFRPMCRPNLRKISTPYVIE 396
OY      407 ICAKHGLSYEVKPELLALVDIVRSLKXS 434
Db      397 LCKHNLPYNVNASFSKANEMTKLRKLRNT 424

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RESULT 14
US-08-789-936-5
Sequence 5, Application US/08789936
Patent No. 5789220

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Avutu S.
APPLICANT: Nocito, Michael
APPLICANT: Freysinet, Georges L.
APPLICANT: Nunberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,936
FILING DATE: 28-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/366,779
FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:

```

? NAME: Presser, Leopold
? REGISTRATION NUMBER: 19,827
? REFERENCE/DOCKET NUMBER: 8382ZYKXMK
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (516) 742-4343
? TELEFAX: (516) 742-4366
? TELEX: 230 901 SANS UR
? INFORMATION FOR SEQ ID NO: 5:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 448 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE:
?
US-08-789-936-5

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Query Match	Similarity	26.8%	Score	4.22	DB 1	Length	448	
Best Local	Similarity	26.8%	Pred. No.	2,8e-37				
Matches	120	Conservative	72	Mismatches	182	Indels	74	Gaps
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QY	26	EQIRAHDPGRKGLVIERKRYDLSKMAQHNHGSGRLIGHGADATDAFAHQ-----	79					
Db	12	DEKKNDHFGDLMSIQGKATVDQMKVQHNHGSPKSTASAGGVDAVAFVHNPASTWKN	71					
QY	80	-DINEVKKFLQPLRIGLAEERPSQDGRILMAQLEDFERALHQAEDMKLFDSPTTFAPL	138					
Db	72	LKRFETGYLLIDVSYSEVS-----KDRKVLVEFGSKMGLDYCK-----	109					
QY	139	LGHL-----AMEVLAILLY--LAPGQVPSALAAFLILASQASQWCLQNDLGHAIFK	191					
Db	110	-GHMFATCFIAMLFAMSYGVLCFEGVILHFRSGCLMGFLIQSGWIGHGHIYVWS	168					
QY	192	KSMNHVNAQKRYVMQDLKGFSAHMHNFQHNARPLFHHDRPYTAARVFLG-----	244					
Db	169	DSRLKKEPMTIANCLSISIGMKKNHNAHNAICNSLETPRDLQYIFPLVYSSKFGSL	228					
QY	245	-----ESSVEYGGKKRRRYRLPYNOOHLRPLGLPRL--TLNFEVENTALYL---VCMQ	293					
Db	229	TSHFETKRLTDSLRFPSYV--QHHTFY-----PIMCARLNNYVOSLMLTLTKRNSYR	282					
QY	294	WADLLMAA--SFYARFLSYLRFYGVPCVLLFPA--VRVLESIMHFWTIOMNHIFKE-	347					
Db	283	AOELLGCLVFETIYRPLLVSCLRPMGBR--IMFVLAISLVGMQVOF-----SLNHSSSV	336					
QY	348	-IGHEKHNDWVSQSLATCNVDSLEFTMVSFGHILNPQIEHHIRPPHRYNSRYAFLYKS	406					
Db	337	YVGRKKGNNMEKQGTQDIDISPRMDMFQSGQFQIENHLFRKAKRQNLKTKSPVYIE	396					
QY	407	LCAKGLSEYKPRFLRALVDYASLKS	434					
Db	397	LCKKHLPYNTAFSSKANEKMTLTPLANT	424					

RESULT 15 34254-5
 US-08-934-254-5
 : Sequence 5, Application US/08934254
 : Patent No. 635861
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: THOMAS, Terry L.
 : TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 : TITLE OF INVENTION: DELTA 6-DESATURASE
 : NUMBER OF SEQUENCES: 27
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Scully, Scott, Murphy & Presser
 : STREET: 400 Garden City Plaza
 : City: Garden City
 : STATE: New York
 : COUNTRY: United States
 : zip: 11530
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 8, 2002, 03:30:16 ; Search time 6458.34 Seconds
(without alignments)
1623.358 Million cell updates/sec

Title: US-09-806-088-1_COPY-9000_9500

Sequence: 501 1 aaaccagactctacgaat.....tgcctcaaaaattttica 501

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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24: em_pl:*
25: em_pi:*
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27: em_pi:*
28: em_pi:*
29: em_pi:*
30: em_pi:*
31: em_pi:*
32: em_pi:*
33: em_pi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C	1	501	100.0	112309	9	AC003025	Human Chr
C	2	501	100.0	133683	2	AC084857	Homo sapi
C	3	501	100.0	138627	2	AP000591	Homo sapi
C	4	501	100.0	142092	2	AF139813	Homo sapi
C	5	501	100.0	196080	9	AC004228	Homo sapi
C	6	295.8	59.0	215936	6	CNS0527C	Homo sapi
C	7	295.4	59.0	191903	9	AC003803	Homo sapi
C	8	294.2	58.7	148984	9	HS105016	Homo sapi
C	9	293.4	58.6	127384	2	AL157823	Homo sapi
C	10	293.4	58.6	159482	2	AL151371	Homo sapi
C	11	292.6	58.6	175989	2	AL590962	Homo sapi
C	12	292.6	58.4	142598	2	AC097104	Homo sapi
C	13	292.6	58.4	163350	2	AC024884	Homo sapi
C	14	292.6	58.3	172159	2	AC017058	Homo sapi
C	15	290	57.9	86196	2	AL592046	Homo sapi
C	16	290	57.9	148429	2	HS103602	Homo sapi
C	17	290	57.9	169913	2	AC031980	Homo sapi
C	18	288.6	57.6	112568	2	AC073886	Homo sapi
C	19	288.6	57.6	194156	2	AC009851	Homo sapi
C	20	288.4	57.6	163166	2	AL356632	Homo sapi
C	21	288	57.5	177893	2	AC108471	Homo sapi
C	22	288	57.5	203038	9	AC076968	Homo sapi
C	23	287.8	57.4	135038	2	AC004000	Homo sapi
C	24	287.6	57.4	128117	2	AC009206	Homo sapi
C	25	287.6	57.4	128117	2	AC009206	Homo sapi
C	26	287.6	57.4	128117	2	AC009206	Homo sapi
C	27	287.6	57.4	128117	2	AC009206	Homo sapi
C	28	287	57.3	158405	2	AC009206	Homo sapi
C	29	287	57.3	158405	2	AC009206	Homo sapi
C	30	287	57.3	158405	2	AC009206	Homo sapi
C	31	286.6	57.2	160017	2	AC027473	Homo sapi
C	32	286.6	57.2	162644	2	AC027473	Homo sapi
C	33	286.6	57.2	162644	2	AC027473	Homo sapi
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C	35	285.8	57.0	157001	2	CNS070E5	Homo sapi
C	36	285.4	57.0	145726	2	AC021807	Homo sapi
C	37	285.4	57.0	145726	2	AC021807	Homo sapi
C	38	285.4	57.0	170528	2	AC083866	Homo sapi
C	39	285.4	56.9	123653	2	AC093268	Homo sapi
C	40	285	56.9	14608	2	AC073620	Homo sapi
C	41	284.8	56.8	110000	2	AL627422-1	Homo sapi
C	42	284.2	56.7	137022	2	AC004231	Homo sapi
C	43	283.6	56.6	105213	2	AL158217	Homo sapi
C	44	283.6	56.6	143065	2	HS20208	Homo sapi
C	45	283.6	56.6	150237	2	AL357335	Homo sapi

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	TITLE	JOURNAL	REFERENCE	AUTHORS
1	AC003025/c	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
2	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
3	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
4	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
5	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
6	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
7	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
8	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
9	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
10	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
11	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
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13	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
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16	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
17	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
18	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
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20	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
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27	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
28	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
29	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
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33	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112309 bp DNA linear PRI 23-JUL-1998	Evans, G.A., Athanasiou, M., Bradbury, P., Brignac, S., Bumeister, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gordon, M.,		
34	AC003025	Human Chromosome 11p12.2 PAC clone pJ466a11, complete sequence.	AC003025	AC003025.1	GI:3337308	HTG.	Human.	112			

TITLE

Submitted (21-Oct-1997) genome science and technology center,
University of Texas Southwestern Medical Center at Dallas, 5323
Harry Hines Blvd, Dallas, TX 75235-8591, USA

REFERENCE

3 (bases 1 to 112309)

AUTHORS

Evans,G.A., Achanasious,M., Aguayo,P., Armstrong,D., Basit,M.,
Buetner,J., Bumeister,R., Card,P., desai,boat,F., Dunn,J.,
English,C., Ehrigide,S., Garner,H.R., gee,V., Gordon,M., Gotway,G.,
Grant,O., Hahner,L., Joslin,J., Lewis,B., Loo,H., Loo,K.N.,
Major,T., McFarland,J., Newton,J., Osborne-Lawrence,S.,
Schageman,J., Schultz,R.A., Stimson,S., Syed,M. and Ward,T.

COMMENT

Submitted (23-Jul-1998) genome science & technology center,
University of Texas Southwestern Medical Center, 5323 Harry Hines
Blvd, Dallas, TX 75235-8591, USA
On Jul 23, 1998 this sequence version replaced g1:2534967.
IMPORTANT: This submission contains the entire insert of clone
pD1466all. pD1466all comes from a PAC library constructed at the
Roswell Park Cancer Institute by the Pieter de Jong group. This
clone has been finished according to strict quality criteria and
attempts have been made to resolve all base calling problems such
as compressions and repetitive elements. The expected Phred/Phrap
calculated errors/10kb is 0.18. In addition, this sequence has
been finished such that 99.9% of consensus base calls consist of
either double-stranded coverage or 2 types of labeling chemistry on
one strand.
Further information regarding the map of this region or
annotation of pD1466all can be found at
<http://gestec.swmed.edu/chromosol.htm>.
CHROMOSOMAL LOCUS: This PAC clone comes from the Chromosome
11p12.2 Best's disease region mapped between STS D11S461 and EST
AHNAK. This region spans over 1.5 Mbp.
MARKER CONFIRMATION: EST: FTH (fertilin heavy chain mRNA)
MAPPED CLONE OVERLAP: HTGS submitted PAC clones pD151913 and
pD1756b9.

FEATURES

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6435	11913: contig of 5479 bp in length
11914	12013: gap of 100 bp
12014	20756: contig of 8743 bp in length
20757	20856: gap of 100 bp
20857	229735: contig of 8879 bp in length
23736	23833: gap of 100 bp
29836	38645: contig of 8810 bp in length
38646	38745: gap of 100 bp
38746	52193: contig of 13448 bp in length
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52294	65208: contig of 12316 bp in length
65210	65308: gap of 100 bp
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79797	79896: gap of 100 bp
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ORIGIN		

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Best Local Similarity 100.0%; Pred. No. 2.6e-148;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT	3
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LOCUS	
DEFINITION	Homo sapiens chromosome 11 clone CMB9-22K5 map 11q13, WORKING DRAFT SEQUENCE, 28 unordered pieces.
ACCESSION	AP000591.3 GI:8118797
VERSION	HTG; HTGS_PHASE1; HTGS_DRAFT
KEYWORDS	Homo sapiens DNA; Clone:CMB9-22K5.
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 138627)
AUTHORS	Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sekaki,Y.
TITLE	Homo sapiens 138,627 genomic DNA of 11q13
JOURNAL	Published Only in Database (1999) In press
REFFERENCE	2 (bases 1 to 138627)
AUTHORS	Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sekaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (12-Oct-1999) Masahira Hattori, The Institute of Physical

COMMENT On May 31, 2000 this sequence version replaced gi:6997481.

----- Genome Center

Center: RIKEN Genomic Sciences Center(GSC)

Center code: RIKEN

Web site: <http://hqp.gsc.riken.go.jp/>

Contact: hattori@qsc.riken.go.jp

----- Protect Information -----

Center project name: HumDraft11

Center clone name: CMB9-22K5

Center Name: CHD, ZKX

--- initially scalar ---

sequencing vector: PCR products,

Chemistry: Dye-terminator E17-amine

Assembly program: Phrap; version:

Consensus quality: 122298 bases

Consensus quality: 130648 bases

Consensus quality: 134094 bases at least Q20
Insert size: 135827; sum-of-contrigs
Quality coverage: 4.01x in Q20 bases; sum-of-contrigs

NOTE: This is a 'working draft' sequence. It currently consists of 28 contrigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contrigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

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46166 46065 contrig of 11299 bp in length
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Sequence updated (20-Oct-1999)
Sequence updated (26-May-2000).

* NOTE: This is a 'working draft' sequence. It currently
* consists of 28 contrigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contrigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```
1 20726 contrig of 20726 bp in length
20827 20826: gap of 100 bp
20827 34666: contrig of 13840 bp in length
34667 34766: gap of 100 bp
34767 46065: contrig of 11299 bp in length
46066 46165: gap of 100 bp
46166 53516: contrig of 7351 bp in length
53517 53616: gap of 100 bp
53617 61065: contrig of 7449 bp in length
61066 61165: gap of 100 bp
61166 67998: contrig of 6833 bp in length
67999 68098: gap of 100 bp
68099 74526: contrig of 6428 bp in length
74527 74626: gap of 100 bp
74627 81299: contrig of 6673 bp in length
81300 81399: gap of 100 bp
81400 87316: contrig of 5917 bp in length
87317 87416: gap of 100 bp
87417 91541: contrig of 4125 bp in length
91542 91641: gap of 100 bp
91642 95731: contrig of 4090 bp in length
95732 95831: gap of 100 bp
95832 101128: contrig of 5297 bp in length
101129 101228: gap of 100 bp
```

FEATURES

```
source
* 101229 104948: contrig of 3720 bp in length
* 104949 105048: gap of 100 bp
* 105049 110306: contrig of 5258 bp in length
* 110307 110406: gap of 100 bp
* 110407 112969: contrig of 2563 bp in length
* 112970 113069: gap of 100 bp
* 113070 116484: contrig of 3415 bp in length
* 116485 116584: gap of 100 bp
* 116585 119599: contrig of 3015 bp in length
* 119600 119699: gap of 100 bp
* 119700 121881: contrig of 2182 bp in length
* 121882 121981: gap of 100 bp
* 121982 122703: contrig of 722 bp in length
* 122704 122803: gap of 100 bp
* 122804 125566: contrig of 2763 bp in length
* 125667 125666: gap of 100 bp
* 125667 126845: contrig of 1179 bp in length
* 126846 126945: gap of 100 bp
* 126946 129349: contrig of 2404 bp in length
* 129350 129449: gap of 100 bp
* 129450 131268: contrig of 1819 bp in length
* 131269 131368: gap of 100 bp
* 131369 132565: contrig of 1197 bp in length
* 132566 132665: gap of 100 bp
* 132666 134031: contrig of 1366 bp in length
* 134032 134131: gap of 100 bp
* 134132 136176: contrig of 2045 bp in length
* 136177 136276: gap of 100 bp
* 136277 137418: contrig of 1142 bp in length
* 137419 137518: gap of 100 bp
* 137519 138627: contrig of 1109 bp in length.

1. 138627
location/Qualifiers
  organism="Homo sapiens"
  db_xref="taxon:9606"
  chromosome="11"
  map="11q13"
  clone="CM99-22K5"

1. 20726
  note="assembly-fragment"
misc_feature
  20827..34666
  note="assembly-fragment"
misc_feature
  34767..46065
  note="assembly-fragment"
misc_feature
  46166..53516
  note="assembly-fragment"
misc_feature
  53617..61065
  note="assembly-fragment"
misc_feature
  61166..67998
  note="assembly-fragment"
misc_feature
  68099..74526
  note="assembly-fragment"
misc_feature
  74627..81299
  note="assembly-fragment"
misc_feature
  81400..87316
  note="assembly-fragment"
misc_feature
  87417..91541
  note="assembly-fragment"
misc_feature
  91642..95731
  note="assembly-fragment"
misc_feature
  95832..101128
  note="assembly-fragment"
misc_feature
  101229..104948
  note="assembly-fragment"
misc_feature
  105049..110306
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misc_feature
  110407..112969
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  113070..116484
  note="assembly-fragment"
misc_feature
  116585..119599
  note="assembly-fragment"
misc_feature
  119700..121881
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|||||
Db 105309 CAAGCTCAGAGGACGTGATTGTCATCATCGACCTGACGCTGACGAGTAGAGCC 105368
QY 481 ctgtctcaaaaaattttca 501
|||||
Db 105369 CTGTCTCAAAAAAATTTTCA 105389

RESULT 5

AC004228/C

LOCUS

AC004228 196080 bp DNA linear PRI 24-FEB-1999

DEFINITION

Homo sapiens Chromosome 11q12.2 PAC clone pDU519013 containing

ACCESSION

AC004228

VERSION

AC004228.2 GI:4263838

KEYWORDS

HTG.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Plimates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 196080)

AUTHORS

Evans,G.A., Athanasiou,M., Basit,M., Bradbury,P., Brignac,S.,

Buetner,J., Buetner,R., Davis,C., English,C., Franklin,T.L., Garner,H.R.,

Gee,V., Gordon,M., Gotway,G., Grant,O., Hahner,L., Harris,J.,

Hinson,S., Narayanaswamy,U., Newton,J., O'Brien,K., Patel,P.,

Schageman,J., Schilling,P., Schultz,R., Syed,M., Valenzuela,D.,

Ward,T. and Wilson,R.

HNGS Submission

TITLE

Unpublished

JOURNAL

2 (bases 1 to 196080)

REFERENCE

Submitted (26-FEB-1998) Genome Science & Technology Center,

AUTHORS

University of Texas Southwestern Medical Center, 5323 Harry Hines

Blvd, Dallas, TX 75235-8591, USA

REFERENCE

3 (bases 1 to 196080)

AUTHORS

Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M.,

Buetner,J., Butler,C., Card,P., desAllbois,F., Dunn,J.,

English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M., Gotway,G.,

Grant,O., Hahner,L., Joslin,J., Lewis,E., Loo,H., Loo,K.N.,

Major,T., McFarland,J., Newton,J., Osborne-Lawrence,S.,

Schageman,J., Schultz,R.A., Stimson,S., Waller,K. and Ward,T.

Direct Submission

TITLE

Submitted (26-FEB-1998) Genome Science & Technology Center,

JOURNAL

University of Texas Southwestern Medical Center, 5323 Harry Hines

Blvd, Dallas, TX 75235-8591, USA

REFERENCE

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AUTHORS

Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M.,

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English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M., Gotway,G.,

Grant,O., Hahner,L., Joslin,J., Lewis,E., Loo,H., Loo,K.N.,

Major,T., McFarland,J., Newton,J., Osborne-Lawrence,S.,

Schageman,J., Schultz,R.A., Stimson,S., Waller,K. and Ward,T.

Direct Submission

TITLE

Submitted (24-FEB-1999) Genome Science & Technology Center,

JOURNAL

University of Texas Southwestern Medical Center, 5323 Harry Hines

Blvd, Dallas, TX 75235-8591, USA

COMMENT

On Feb 24, 1999 this sequence version replaced gi:2911733.

IMPORTANT: This submission contains the entire insert of clone

pDU519013. pDU519013 comes from the RPCT-3 PAC library constructed

at the Roswell Park Cancer Institute by the Pister de Jong group.

CHROMOSOMAL LOCUS: This PAC clone comes from the Chromosome

11p12.2 Best's disease region mapped between STS D11S461 and EST

AHNAK. This region spans over 1.5 Mbp.

MARKER CONFIRMATION: EST; FTH (ferritin heavy chain mRNA), STS

D11S699 and WI-7524

MAPPED CLONE OVERLAP: PACs pDU466a11 and pDU756b9.

FEATURES

SOURCE

Location/Qualifiers

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/Organism="Homo sapiens"

/db_xref="taxon:9606"

complement(2210..2482)

repeat_region

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3457..3743

/rpt_family="Alu"

repeat_region

/rpt_family="Alu"

complement(20145..20758)

repeat_region

/rpt_family="Alu"

complement(23194..23599)

repeat_region

/rpt_family="Alu"

repeat_region complement(27367..27685)

/rpt_family="Alu"

28047..28457

repeat_region /rpt_family="Alu"

complement(29390..29565)

/rpt_family="Alu"

complement(31076..31255)

/rpt_family="Alu"

complement(34948..35045)

/rpt_family="Alu"

35232..35538

repeat_region /rpt_family="Alu"

complement(36242..36540)

/rpt_family="Alu"

37238..37522

repeat_region /rpt_family="Alu"

complement(38555..38650)

/rpt_family="Alu"

complement(40483..41164)

/rpt_family="Alu"

42042..42116

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42677..42817

/rpt_family="LFR12"

42856..43157

repeat_region /rpt_family="Alu"

43148..43380

repeat_region /rpt_family="LFR12"

complement(43738..43999)

/rpt_family="LFR12"

complement(46998..47169)

/rpt_family="MIR"

complement(48048..48346)

/rpt_family="Alu"

48482..48737

repeat_region /rpt_family="Alu"

complement(48893..49037)

/rpt_family="L1"

49118..49292

repeat_region /rpt_family="Alu"

49791..50059

/rpt_family="Alu"

50436..50501

repeat_region /rpt_family="Alu"

complement(51147..51441)

/rpt_family="Alu"

complement(52700..52979)

/rpt_family="Alu"

53281..53568

repeat_region /rpt_family="Alu"

54071..54204

repeat_region /rpt_family="Alu"

54506..54793

repeat_region /rpt_family="Alu"

54807..55061

repeat_region /rpt_family="Alu"

complement(64533..64826)

/rpt_family="Alu"

complement(65245..65783)

/rpt_family="Alu"

complement(68465..68732)

/rpt_family="Alu"

complement(70191..70476)

/rpt_family="Alu"

70560..70692

repeat_region /rpt_family="Alu"

72294..72470

repeat_region /rpt_family="Alu"

complement(72800..73095)

/rpt_family="Alu"

73424..73695

repeat_region /rpt_family="Alu"

73784..74071

repeat_region

OY	61	ccacaccatcagcttaggtcaaggacaagaattcttgaaccttgagggagtgcattgca	120
Db	111845	CCCACTACTACATTAAGGCTTAGGGCACAAGAATCTTTCAACTGGAGGTGGAGATTGCA	111786
OY	121	gtaaoccgatacatgccaactgcaaacccagtccttgggcgacagagcaagactctgtctcaa	180
Db	111785	GTAAGCGGAATCATGCCACTGCACCAACCAGTCTGGGGCCACAGACAAAGCTCTGTTCTCAA	111726
OY	181	aaaataaagataaataaaaaatttagagggccaggtgtgagttcacaccttatcttaacac	240
Db	111725	AAAATAAATAATTAATTAATAAATTAATTAAGAGCCAGGTGTGGTGCTCACACCTGTACTCTAAC	111666
OY	241	actttgggaagcttgaggtgggagagatcgcttgaagtcagagcatttaagacatgcctaaggc	300
Db	111665	ACTTTGGAGAGCTGAGAGGTGGAGGATTCGGTTGMAATCTAGGCAATTAAGACATCCATAGGC	111606
OY	301	aacatatgagaccttgaactctacaaaaaaattcaaaagttaatgagacatgtgtgcatg	360
Db	111605	AACATATGAGACCTTGTGACTCTACAAAAAAATTCAAAAGTTTAATGACACATGTGTGGCATTG	111546
OY	361	tgcctgtagcttagctagctgtctgtggggaagcttgaggtvggagatcaacttaagcagaattt	420
Db	111545	TGCTGTAGTGCCTTAGCTGTGGGGAGCTGAGAGTGGGAGATCTTAACACACAGGATATT	111486
OY	421	caagctgcacgctagctgtgatgtgcatcaactcgaactccagcctgtgtgacagagtgaagcc	480
Db	111485	CAAAGCTGCAGTAGTAGCGTGTGATTTGCATCTCATCTGCATCTCCAGCTCTGGTGCACAGATGAGGCC	111426
OY	481	ctgtctctaaaaaaatttttca 501	
Db	111425	CTGTCTCAAAAAAAATTTTCA 111405	
RESULT	6		
CNS05TCA		215936 bp DNA linear PRI 24-sep-2001	
LOCUS		Human chromosome 14 DNA sequence BAC C-2509G16 of library CalTech-D-	
DEFINITION		From chromosome 14 of Homo sapiens (Human), complete sequence.	
ACCESSION		AL355076	
VERSION		AL355076.5 GI:15617343	
KEYWORDS		HFG.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE		1 (bases 1 to 215936)	
JOURNAL		Heilig/R., Pettit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,	
REFERENCE		Brotier/P., Cellotello,L., Barbe,V., Pelletier,E., Artiguenave,F.,	
AUTHORS		Ley,M., Eckenberg,R., Bruls,T., debernardinis,V., Gruaud,C.,	
JOURNAL		Gyapay,G., Saurin,W. and Weissenbach,J.	
REFERENCE		Sequencing of the human chromosome 14	
TITLE		Unpublished	
DATE		2 (bases 1 to 215936)	
GENOSCOPE		Genoscope.	
DIRECT SUBMISSION		Direct Submission	
Submitted (24-Sep-2001) Genoscope - Centre National de Sequencage :			
Bp 191 91006 EVRY cedex - FRANCE (E-mail : segrel@genoscope.cns.fr			
- Web : www.genoscope.cns.fr)			
On Sep 13, 2001 this sequence version replaced gi:14494870.			
----- Genome Center -----			
Center: Genoscope / Centre National de Sequencage			
Center code: GS			
Web Site: http://www.genoscope.cns.fr/			
Contact: Segrel@genoscope.cns.fr			

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-840119
Downstream BAC (overlapping the SP6 end) : R-960H4 (AC=AL359236)

```

Assembly program: Phrap; version 2.0
Quality coverage: 6.41x in Q20 bases; sum-of-contigs
-----

```


repeat_region	/note="AluSx repeat: matches 1. .236 of consensus"
repeat_region	17546. .17703 repeat: matches 61. .226 of consensus"
repeat_region	/note="MIR repeat: matches 61. .226 of consensus"
repeat_region	17736. .17993 repeat: matches 5889. .6148 of consensus"
repeat_region	/note="L1PA9 repeat: matches 5889. .6148 of consensus"
repeat_region	18033. .18340 repeat: matches 1. .310 of consensus"
repeat_region	/note="AluSx repeat: matches 1. .310 of consensus"
repeat_region	18509. .18757 repeat: matches 6. .271 of consensus"
repeat_region	/note="AluSg repeat: matches 6. .271 of consensus"
repeat_region	19384. .19412 repeat: matches 236. .262 of consensus"
repeat_region	/note="MIR repeat: matches 236. .262 of consensus"
repeat_region	19413. .19624 repeat: matches 171. .364 of consensus"
repeat_region	/note="THE1B repeat: matches 171. .364 of consensus"
repeat_region	19625. .19928 repeat: matches 1. .304 of consensus"
repeat_region	/note="AluSx repeat: matches 1. .304 of consensus"
repeat_region	19929. .20091 repeat: matches 3. .171 of consensus"
repeat_region	/note="THE1B repeat: matches 3. .171 of consensus"
repeat_region	20092. .20260 repeat: matches 53. .236 of consensus"
repeat_region	/note="MIR repeat: matches 53. .236 of consensus"
repeat_region	20551. .20974 repeat: matches 27. .532 of consensus"
repeat_region	/note="MIR repeat: matches 27. .532 of consensus"
repeat_region	21157. .21452 repeat: matches 24. .311 of consensus"
repeat_region	/note="AluSx repeat: matches 24. .311 of consensus"
repeat_region	21600. .21740 repeat: matches 1. .139 of consensus"
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repeat_region	21741. .22035 repeat: matches 1. .295 of consensus"
repeat_region	/note="AluSg repeat: matches 1. .295 of consensus"
repeat_region	22036. .22175 repeat: matches 133. .286 of consensus"
repeat_region	/note="AluSx repeat: matches 133. .286 of consensus"
repeat_region	22470. .22618 repeat: matches 7822. .7974 of consensus"
repeat_region	/note="L1MK4 repeat: matches 7822. .7974 of consensus"
repeat_region	22641. .22841 repeat: matches 129. .303 of consensus"
repeat_region	/note="AluMb repeat: matches 129. .303 of consensus"
repeat_region	22842. .23150 repeat: matches 1. .301 of consensus"
repeat_region	/note="AluSg repeat: matches 1. .301 of consensus"
repeat_region	23151. .23270 repeat: matches 3. .129 of consensus"
repeat_region	/note="AluMb repeat: matches 3. .129 of consensus"
repeat_region	23315. .23399 repeat: matches 7552. .7843 of consensus"
repeat_region	/note="L1MK4 repeat: matches 7552. .7843 of consensus"
repeat_region	23603. .23898 repeat: matches 4. .299 of consensus"
repeat_region	/note="AluMo repeat: matches 4. .299 of consensus"
repeat_region	23903. .24125 repeat: matches 47. .300 of consensus"
repeat_region	/note="AluMo repeat: matches 47. .300 of consensus"
repeat_region	24130. .24308 repeat: matches 7377. .7560 of consensus"
repeat_region	/note="L1MK4 repeat: matches 7377. .7560 of consensus"
repeat_region	24845. .25372 repeat: matches 5380. .5809 of consensus"
repeat_region	/note="L1ME repeat: matches 5380. .5809 of consensus"
repeat_region	25331. .25333 repeat: matches 1. .303 of consensus"
repeat_region	/note="AluSx repeat: matches 1. .303 of consensus"
repeat_region	25655. .25939 repeat: matches 1. .285 of consensus"
repeat_region	/note="AluSg repeat: matches 1. .285 of consensus"
repeat_region	25940. .25999 repeat: matches 12 mer 85% conserved"
repeat_region	/note="5 copies 12 mer 85% conserved"
repeat_region	26201. .26500 repeat: matches 2. .135 of consensus"
repeat_region	/note="AluSx repeat: matches 2. .135 of consensus"
repeat_region	26570. .26703 repeat: matches 1. .302 of consensus"
repeat_region	/note="F1ALC repeat: matches 1. .302 of consensus"
repeat_region	26846. .27142 repeat: matches 5. .387 of consensus"
repeat_region	/note="AluSx repeat: matches 5. .387 of consensus"
repeat_region	27346. .27712 repeat: matches 1. .127 of consensus"
repeat_region	/note="L1TR16C repeat: matches 1. .127 of consensus"
repeat_region	28454. .28600 repeat: matches 1. .306 of consensus"
repeat_region	/note="AluMo repeat: matches 1. .306 of consensus"
repeat_region	28601. .28906 repeat: matches 127. .298 of consensus"
repeat_region	/note="AluMo repeat: matches 127. .298 of consensus"
repeat_region	28907. .29071 repeat: matches 2. .31 of consensus"
repeat_region	/note="Chenille repeat: matches 2. .31 of consensus"
repeat_region	29129. .29437 repeat: matches 1. .309 of consensus"
repeat_region	/note="AluSx repeat: matches 1. .309 of consensus"

Best Local Similarity 76.0%; Pred. No. 1,5e-82;
Matches 376; Conservative 0; Mismatches 118; Indels 1; Gaps 1;

[illegible]

RESULT	9
AL157823/c	
LOCUS	127384 bp DNA linear PRI_10-FEB-2001
DEFINITION	Human DNA sequence from clone RP3-51008 on chromosome 6, complete sequence.
ACCESSION	AL157823
VERSION	AL157823.9 GI:12750800
KEYWORDS	HFG.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. I (Passes I to 127384)
REFERENCE	Williams,S. Direct Sublssion Submitted (10-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk On Feb 12, 2001 this sequence version replaced gi:12709859.
AUTHORS	
JOURNAL	
TITLE	
COMMENT	

variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >30); an attempt was made to resolve all sequencing problems, such as compressions and repeats: all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given

Query Match

58.78; Score 294.2; DB 9; Length 148984;

abbreviations are used to associate primary accession numbers given

RESULT	12	142598 bp	DNA	linear	HTG 31-JAN-2002
LOCUS	AC097104/c				WORKING DRAFT
DEFINITION	AC097104	142598 bp	DNA	linear	HTG 31-JAN-2002
ACCESSION	AC097104	142598 bp	DNA	linear	HTG 31-JAN-2002
VERSION	AC097104.3	142598 bp	DNA	linear	HTG 31-JAN-2002
KEYWORDS	HTG; PHASE1; HTGS_DRAFT.				
SOURCE	human.				
ORGANISM	Human sapiens				
REFERENCE	1 (bases 1 to 142598)				
AUTHORS	Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alshrooks, S.L., Amarantunga, H.C., Arc, J.R., Ayale, M., Banks, T., Barbieri, J., Benton, J., Bimarge, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowles, B., Brivea, M., Brown, E., Brown, M., Bryant, N.P., Bushy, C., Burck, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dahorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dedertch, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Ellis, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisl, J.H., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlik, P., Hayes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudash, S., Karlsson, E., Kelly, S., Khan, U., King, L., Koryah, J., Kovar, C., Kralovic, J., Kireshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louisedge, H., Lozados, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheswari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Maxwell, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nicholson, E., Niochenko, S., Ogun, M., Okunou, G., Oragunye, N., Oyiedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojudo, K., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoostali, N., Sisson, I., Soderey, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Swatek, A., Tabors, P., Tameris, A., Tameris, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, R., Woodson, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.				
TITLE	Direct Submission				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 142598)				
AUTHORS	Worley, K.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (09-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA				
COMMENT	On Jan 31, 2002 this sequence version replaced gi:11760999.				
	Genome Center				
	Center: Baylor College of Medicine				
	Center code: BCM				
	Web site: http://www.hgsc.bcm.tmc.edu/				
	Contact: hgsc-help@bcm.tmc.edu				
	Project Information				
	Center project name: HCOH				
	Center clone name: RP11-153M3				
	Sequencing vector: Plasmid; M77789				

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Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly: Phrap; version 0.990329First call to
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Consensus quality: 139529 bases at least Q20
Estimated insert size: 136972; sum-of-contris estimation
Quality coverage: 0x in Q20 bases; agrose-1p estimation
Quality coverage: 3.4x in Q20 bases; sum-of-contris estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html)
* NOTE: This is a 'working draft' sequence. It currently
* consists of 27 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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TITLE Fitzpatrick, E.S., Harrison, K.M., Petrukhin, K., Caskey, C.T. and Merker, M.L.
JOURNAL Submitted (01-APR-1999) Department of Human Genetics, Merck & Co., Inc., Sumneytown Pike, West Point, PA 19486, USA
REMARK IMPORTANT: This submission contains the entire insert of clone PDJ75912 which comes from a PAC library constructed at the Roswell Park Cancer Institute by the Pieter de Jong group. This clone has been finished according to strict quality criteria and attempts have been made to resolve all base calling problems such as compressions and repetitive elements. This sequence has been finished such that all consensus base calls consist of two or more separate clones with double-stranded coverage or two or more separate clones with two types of sequencing chemistry. The expected Phred/Phrap calculated errors/10kb is 0.00.

FEATURES

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RESULT 3
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SOURCE human.
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 112309)
AUTHORS Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basil,M.,
Buettnier,J., Bumeister,R., Card,P., deSallibaat,F., Dunn,J.,
English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M., Gotway,G.,
Major,O., Mahner,L., Joslin,J., Lewis,E., Loo,H., Loo,K.N.,
Major,T., McFarland,J., Newton,J., Osborne-Lawrence,S.,
Schageman,J., Schultz,R.A., Stimson,S., Syed,M. and Ward,T.
HTGS Submission
TITLE Unpublished
JOURNAL 2 (bases 1 to 112309)
AUTHORS Evans,G.A., Athanasiou,M., Bradbury,P., Brignac,S., Bumeister,R.,
Davis,C., English,C., Franklin,T.L., Garner,H.R., Gordon,M.,
Gotway,G., Grant,O., Hahner,L., Harris,J., Hinson,S.,
Narasanaswamy,U., Newton,J., O'Brien,K., Oliver,T., Patel,P.,
Probst,S., Rayner,S., Schageman,J., Schilling,P., Schultz,R.,
Syed,M., Valenzuela,D., Ward,T. and Wilson,R.
Direct Submission
TITLE Submitted (21-OCT-1997) Genome Science and Technology Center,
JOURNAL University of Texas Southwestern Medical Center at Dallas, 5323
HARRY HINES BLVD, DALLAS, TX 75235-8591, USA
3 (bases 1 to 112309)
AUTHORS Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basil,M.,
Buettnier,J., Bumeister,R., Card,P., deSallibaat,F., Dunn,J.,
English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M., Gotway,G.,
Grant,O., Hahner,L., Joslin,J., Lewis,E., Loo,H., Loo,K.N.,
Major,T., McFarland,J., Newton,J., Osborne-Lawrence,S.,
Schageman,J., Schultz,R.A., Stimson,S., Syed,M. and Ward,T.

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TITLE Direct Submission
JOURNAL Submitted (23-JUL-1998) Genome Science & Technology Center,
University of Texas Southwestern Medical Center, 5323 Harry Hines
Blvd, Dallas, TX 75235-8591, USA
COMMENT On Jul 23, 1998 this sequence version replaced gi:2554967.
IMPORTANT: pdu46a11 comes from a PAC library constructed at the
Roswell Park Cancer Institute by the Pieter de Jong group. This
clone has been finished according to strict quality criteria and
attempts have been made to resolve all base calling problems such
as compressions and repetitive elements. The expected Pfrd/Pfrap
calculated errors/10kb is 0.18. In addition, this sequence has
been finished such that 99.9% of consensus base calls consist of
either double-stranded coverage or 2 types of labeling chemistry on
one strand.
Further information regarding the map of this region or
annotation of pdu46a11 can be found at
http://gestec.swmed.edu/chromosome1.htm.
CHROMOSOMAL LOCUS: This PAC clone comes from the Chromosome
11p12.2 best's disease region mapped between STS D11S461 and EST
AHNAK. This region spans over 1.5 Mbp.
MARKER CONFIRMATION: EST: FTH (ferritin heavy chain mRNA)
MAAPPED CLONE OVERLAP: HTGS submitted PAC clones pdu519613 and
pdu756b9.
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repeat_region /rpt_family="Alu"
complement(21374..21661)
repeat_region /rpt_family="Alu"
22809..23212
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23499..23752
repeat_region /rpt_family="Alu"
24118..24472
repeat_region /rpt_family="Alu"
25005..25113
repeat_region /rpt_family="MIR"
31160..31442
repeat_region /rpt_family="Alu"
complement(32631..32947)
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complement(35970..36025)
repeat_region /rpt_family="MIR"
38958..39145
repeat_region /rpt_family="Alu"
44878..45480
repeat_region /rpt_family="Alu"
49769..50071
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repeat_region      /rpt_family="MIR"      51038. .51659
repeat_region      /rpt_family="Alu"      54494. .54769
repeat_region      /rpt_family="Alu"      55529. .55623
repeat_region      /rpt_family="THER1"     .55967
repeat_region      /rpt_family="Alu"      56721. .57100
repeat_region      /rpt_family="Alu"      58402. .58680
repeat_region      /rpt_family="Alu"      59345
repeat_region      /rpt_family="Alu"      59678. .59904
repeat_region      /rpt_family="Alu"      61149. .61424
repeat_region      /rpt_family="Alu"      62242
repeat_region      /rpt_family="Alu"      62276. .62710
repeat_region      /rpt_family="MLT1"      62915. .63118
repeat_region      /rpt_family="Alu"      63439. .64614
repeat_region      /rpt_family="Alu"      64984
repeat_region      /rpt_family="Alu"      65596. .65811
repeat_region      /rpt_family="Alu"      66500. .66753
repeat_region      /rpt_family="Alu"      67311. .67542
repeat_region      /rpt_family="Alu"      67835. .68119
repeat_region      /rpt_family="Alu"      68860. .69150
repeat_region      /rpt_family="Alu"      69164. .69272
repeat_region      /rpt_family="Alu"      69354. .70245
repeat_region      /rpt_family="Alu"      70655. .70939
repeat_region      /rpt_family="Alu"      70933. .71075
repeat_region      /rpt_family="L1"      71119. .71395
repeat_region      /rpt_family="Alu"      71404. .71530
repeat_region      /rpt_family="L1R5"      71536. .71637
repeat_region      /rpt_family="L1R5"      72720. .72948
repeat_region      /rpt_family="L1"      73633
repeat_region      /rpt_family="Alu"      73925. .74200
repeat_region      /rpt_family="Alu"      75721. .75955
repeat_region      /rpt_family="Alu"      77185. .77449
repeat_region      /rpt_family="Alu"      78093. .78222
repeat_region      /rpt_family="L1"      78227. .78294
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repeat_region      complement(80458. .80707)
repeat_region      /rpt_family="Alu"      complement(81544. .81974)
repeat_region      /rpt_family="Alu"      82055. .82305
repeat_region      /rpt_family="Alu"      82514. .83096
repeat_region      /rpt_family="Alu"      complement(83685. .83940)
repeat_region      /rpt_family="Alu"      83536. .85850
repeat_region      /rpt_family="Alu"      complement(86429. .86483)
repeat_region      /rpt_family="MIR"      86902. .87183
repeat_region      /rpt_family="Alu"      87646. .87792
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Query Match 97.6%; Score 585.8; DB 9; Length 112309;
Best Local Similarity 99.5%; Pred. No. 3,7e-65;
Matches 598; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 1 gctcaaacaccgagctcccgctccggttccgaagagcgctgagagcgacg 60
DB 21047 gctcACAGACCGGACTCCGCTCCGCTCCGAGGCGGTGCGAGCGC 20988
QY 61 ccaaaagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120
DB 20987 cCAACAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 20928
QY 121 gccgagcagcccgagaaagagagagagagagagagagagagagag 180
DB 20927 GCCGACACCCCGGAGAAAGGCGGAGAGAGAGAGAGAGAGAGAGAG 20868
QY 181 ctgtctcccgagagagagagagagagagagagagagagagagagag 240
DB 20867 CTGTCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 20808
QY 241 cgaagcccgagcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 299
DB 20807 CGAGGCCCCCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 20748
QY 300 cctgagcgagagagagagagagagagagagagagagagagagag 359
DB 20747 CCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 20688
QY 360 cggagaggttccctgagcgagcgagcgagcgagcgagcgagcgag 419
DB 20687 CGGGAGTTCCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 20628
QY 420 gcaagagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 479
DB 20627 GGCAGAGGCGGCGGCGGAGCAGCGGCGGCGGCGGCGGCGGCGGCG 20568
QY 480 ttccctcgaggtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 539
DB 20567 TTCCTCGGGGTCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 20508
QY 540 cagcagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcg 599
DB 20507 CAGCATGGCGGCGTCCGGAGACCGGAGCGGAGCGGAGCGGAGCGGAG 20448
QY 600 g 600
DB 20447 G 20447
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RESULT 4
AC084857 AC084857 133683 bp DNA linear HTG 22-NOV-2000
LOCUS Homo sapiens chromosome 11 clone CTD-323J1NS map 11, WORKING DRAFT
DEFINITION SEQUENCE, 13 unordered pieces.


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Db 41332 CTGTCTCTCCGGAGGGGCGGGCCCTCTGACGCGCCCTCTGCGGGCCAAAGGAGAC 41273
QY 241 cgaagcccgccgcttgatltgaagcgaagc-aggagtcgaagcagccttgaggcgaagc 239
Db 41272 CGAGGCCCGCGGCTTGATGTGAGGAGGAGCGGGGGGTCAACGACCTTGGGGGCGGGG 41213
QY 300 cctgagccgggggggggggggagcagagcgaagcggcgctgcgcgaggtataaag 359
Db 41212 CCTGCCCCGGGGGGGGGGGAGCGAGGCGAGGCGGGGCGCTGCTCCGCGCTTATAGG 41153
QY 360 cggagagttccctgcgcgcgaagcgaagcgaagcgcgcgtcgtacgaagcgcgcgcgc 419
Db 41152 CGGGAGGTTCCCTGCGCGCGGAGCGCGGGAGGCGACGCTGCTGTACGCGGGCGGGGCG 41093
QY 420 ggcagagcgaggcgagcgaagcgaagcgaagcgaagcgcgcgcgcgcgcgcgcgcgcgc 479
Db 41092 GCGAGGCGCGGGCGCGGAGCAGCGGCGCGGCGCGGCGCGCGCGCGCTCTTCGC 41033
QY 480 ttccctgggggtctgtctgcgaagcctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 539
Db 41032 TTCCCTCGGGGCTTGTGCTGGACCTCGGCGACCGCTTGGAATCCCAAGACTCGTGCCTG 40973
QY 540 cagcatggcgagcgtcggaggagcgcggagcgcggaggagagcgcgcgcgcgcgcgcgcgcgc 599
Db 40972 CAGCATGGCGGCGCTCGGGAGACCGCGAGCGCGGAGGAGACCGCGCAGCGCGGGGCGAC 40913
QY 600 g 600
Db 40912 G 40912
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RESULT 5
LOCUS HSA326485/c 629 bp DNA linear PRI 01-OCT-2001
DEFINITION Homo sapiens genomic sequence surrounding Not1 site, clone
ACCESSION AJ326485
VERSION AJ326485.1 GI:15870879
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 629)
AUTHORS Kutsenko,A.S., Gizacullin,R.Z., Al-Amh,A.N., Wang,F.,
Podowski,R.M., Matushkin,Y.G., Kwasha,S.M., Gyanchandani,A.,
Muravenko,O.V., Protodopov,A.I., Kashuba,V.I., Kisselev,L.L.,
Wasserman,M., Wahlstedt,C. and Zabarovsky,E.R.
TITLE Analysis of Not1 flanking sequences: a new tool for gene discovery
and verification of the human genome
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 629)
AUTHORS Zabarovsky,E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumoriology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden
FEATURES
source Location/Qualifiers
1..629
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NRI-EJ1C"
BASE COUNT 70 a 257 c 216 g 86 t
ORIGIN
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Query Match 69.1%; Score 414.4; DB 9; Length 629;
Best Local Similarity 99.8%; Pred. No. 4.8e-43;
Matches 415; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 gctcacagccggagctccgctcgggtccgagggcggtgagagcgctcgaggagc 60
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Db 416 GCTCACAGACCGGAGACTCCGCTCCGCTCCGAGAGGCGTGGCAGAGCCCTCGGGAACGC 357
QY 61 ccaacagtgctgtgtgtgtcccaagagcccgctcgcgggtgagtcgaagccttgaa 120
Db 356 CCACAGAGTGGCTGTGTGTCCCAAGAGCCCGCGCTCCGGGTGAGTCACAGAGCCTGGAA 297
QY 121 gccggcagcccggaagaggggggggggggggggggggggggggggggggggggggggggggg 180
Db 296 GCGGCGAGCCCGGAGAGAGGGGGGCGAGACGTGCTCCCGGGGAGAGCTTGAGTGGCGCGG 237
QY 181 ctgtcctccggaggaggcgaggcgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 240
Db 236 CTGTCTCTCCGGAGGCGGGCGCGGCGCGCTGACGCGCCCTCTGCGCGCCAAAGGAGAGAC 177
QY 241 cgaagcccgccgctgagttgagcgaagcgaagcgaagcgaagcgcgcgcgcgcgcgcgcgcgc 300
Db 176 CGAGGCCCCCGGCTGTGAGAGGAGCGGGGGGTACGACCTTGGGGCGGGGCG 117
QY 301 ctggcgggggggggggggggggggggggggggggggggggggggggggggggggggggggggg 360
Db 116 CTGGCGGGGGGGGGGGGGGAGCGAGGCGAGGCGGGGCGCGCTCCGCGGGTATAAGGC 57
QY 361 gggagagttccctgcgcgcgaagcgcggaggagcgacgcctgcgtacgcgcgcgcgcgcgc 416
Db 56 GGGAGGTTCCCTGCGCGCGGAGCGGAGCGCGACGCTGCTGTACGGCGGCGC 1
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RESULT 6
LOCUS BC004901 1816 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, fatty acid desaturase 3, clone MGC:4158
ACCESSION BC004901
VERSION BC004901.1 GI:13436175
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1816)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
Contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IRAL Plate: 11 Row: B Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4868365.
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="locusid:3995"
/db_xref="taxon:9606"
/clone="MGC:4158 IMAGE:3532219"
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/clone_lib="NIH MGC-17"
/lab_host="DH10B-R"
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CDS

163..1500

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VPSALAAFLTAISOQSWCLOHDLGHASIFKRSWNHVAOKFVWGOLKGFSAHMMNR
HFQHNKRNIFHKDPDVTVAPEVLIGSESVSEYGRKKRRYLPYNOHLFFPLIGPPLT
LVNFEVENLAAYLVCMOMADLMAASFAARPELSYLPFGVGVGLFVAARVLESIM
FVMTQMNHIPEKIGHEKRDWVSQSLAATCNVPSLFTNMFSGHLNFOIENHLFPRM
PRNKSRAVPLVKSICAKKHOLSYEVKPEPLTALVDIVRSLSKSGDIWDALYHQ"

BASE COUNT 351 a 592 c 528 g 345 t

ORIGIN

Query Match 35.4%; Score 212.6; DB 9; Length 1816;

Best Local Similarity 98.2%; Pred. No. 4.1e-18;

Matches 215; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1 GGCACGAGGCGCACGCTGCTCTACGGCGCGCGCGGCAAGGCGGCGCGGAGCAGC 60

QY 382 gccggagggcgagcagctcgtctgtaaggcgccgagcgagcgagcgagcgagcgagc 441

Db 1 GGCACGAGGCGCACGCTGCTCTACGGCGCGCGCGGCAAGGCGGCGCGGAGCAGC 60

QY 442 gggcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 501

Db 61 GGGGGGGGGGAGGAGGCGGCGCGCGGCGGAGGCGGCGGCGGAGCAGC 120

QY 502 cctcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 561

Db 121 CCTCGGCGCACGCGCTGGGATCCCGACGACCTGCGTGCAGCATGGCGCGCGCTCGGGGAG 180

QY 562 ccgggagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 600

Db 181 CCGGGACCGCGGAGGAGCAGCGGCGGAGCAGCGGCGGAGCAGC 219

RESULT 7

LOCUS AX035942 1757 bp DNA linear PAT 15-NOV-2000

DEFINITION Sequence 3 from Patent EP1035207.

ACCESSION AX035942

VERSION AX035942.1 GI:1191484

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 1757)

AUTHORS Marguardt, A. and Weber, B. H.

TITLE Cdna molecules of the members of gene family encoding human fatty acid desaturases and their use in diagnosis and therapy

JOURNAL Patent: EP 1035207-A 3 13-SEP-2000;

FEATURES

location/Qualifiers

1..1757

/organism="unidentified"

/db_xref="taxon:32644"

BASE COUNT 318 a 580 c 517 g 342 t

ORIGIN

Query Match 31.4%; Score 188.4; DB 6; Length 1757;

Best Local Similarity 99.5%; Pred. No. 4.2e-15;

Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 411 ggcgcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 470

Db 1 GGCAGGCGGCGGAGGCGGCGGAGGCGGCGGCGGCGGAGGCGGCGGCGGAGC 60

QY 471 gctctcgcttcctcgaggtctgtctgagactcgagcagcgagcgagcgagc 530

Db 61 GCTCTTCGCTTCCTCGGGGCTTGTGTCGAGCCTCGGCCACCGCTGATCCCGAGGAC 120

QY 531 tcgtcgtgcagcatggcgagcgagcgagcgagcgagcgagcgagcgagcgagc 590

Db 121 TCGTCGTGTCAGCATATGGCGGCGGTGGGAGCGCGGAGCGGAGGAGCAGCGCGCAGCC 180

QY 591 gggggcgagc 600

Db 181 GGGGGCAGCCG 190

RESULT 8

AF084560

LOCUS AF084560 1757 bp mRNA linear PRI 12-OCT-2000

DEFINITION Homo sapiens fatty acid desaturase 3 (FADS3) mRNA, complete cds.

ACCESSION AF084560

VERSION AF084560.1 GI:10798852

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 1757)

Marguardt, A., Stoeck, H., Passmore, L. A., Kraemer, F., Rivera, A. and Weber, B. H. F.

Direct Submission

Submitted (05-AUG-1998) Institute of Human Genetics, University of Wuerzburg, Biozentrum, Am Hubland, Wuerzburg D-97074, Germany

TITLE

three members of the human fatty acid desaturase family

JOURNAL

Genomics 66 (2), 175-183 (2000)

MEDLINE

20318619

PUBMED

10860662

REFERENCE

2 (bases 1 to 1757)

Marguardt, A., Stoeck, H., Passmore, L. A., Kraemer, F., Rivera, A. and Weber, B. H. F.

Direct Submission

Submitted (05-AUG-1998) Institute of Human Genetics, University of Wuerzburg, Biozentrum, Am Hubland, Wuerzburg D-97074, Germany

FEATURES

location/Qualifiers

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/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="11"

/map="11q12-q13.1"

1..1757

/gene="FADS3"

1..133

/gene="FADS3"

74..451

/gene="FADS3"

/note="similar to EST cb98h06.s1 denoted by GenBank

Accession Number AA04782"

134..1471

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/codon_start=1

/product="fatty acid desaturase 3"

/protein_id="AA023122.1"

/db_xref="GI:10798853"

/translation="MGVGEPRGPRGPAQAPLPFTCEQIRAHDPQDKWYIER
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QDGPLNAQLVEDPRAHQAEADMLFDSPPEFAFLIGHILAMEVLAWLILYLGPGW
VPSALAAFLTAISOQSWCLOHDLGHASIFKRSWNHVAOKFVWGOLKGFSAHMMNR
HFQHNKRNIFHKDPDVTVAPEVLIGSESVSEYGRKKRRYLPYNOHLFFPLIGPPLT
LVNFEVENLAAYLVCMOMADLMAASFAARPELSYLPFGVGVGLFVAARVLESIM
FVMTQMNHIPEKIGHEKRDWVSQSLAATCNVPSLFTNMFSGHLNFOIENHLFPRM
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1472..1757

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1738..1743

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/note="variant ATTAAA"

BASE COUNT 318 a 580 c 517 g 342 t

ORIGIN

Query Match 31.4%; Score 188.4; DB 9; Length 1757;

Best Local Similarity 99.5%; Pred. No. 4.2e-15;


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ORIGIN
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Best Local Similarity 96.1%; Pred. No. 1,5e-12;
Matches 174; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db    181 GCTCAGACAGCCGGGAGCTCCGCCTCGGGTTCGCCGAGGCGCTGGAGAGCGCTGCGGAGCAC 122
      |||
QY    61 ccaacagtgtgattttgtgccccaagccccgcgcgtccggttgtagtcagaagcctcgaaa 120
Db    121 CCAACAGTGCGGTGTGTGTGTGCCAGGACCAGCCGCTCCGGGTGAGTCAAGACCTGTCCA 62
      |||
QY    121 gccggcagccccggaaaaaagggggagcaggtgtgcccgaggcagggtctggttcggcg 180
Db    61 GCCCGACAGACCGGGGAAAAGGGGCGGAACGGTCCCCCAGGCGAGCGCTGCTGACCGCCG 2
      |||
QY    181 c 181
Db    1 c 1

RESULT 13
AFI34404      1705 bp     mRNA       linear     PRI 19-MAY-1999
LOCUS         Homo sapiens delta-6 fatty acid desaturase (CYB5RP) mRNA, complete
DEFINITION   cds.
ACCESSION    AFI34404
VERSION      AFI34404.1 GI:4868365
KEYWORDS
SOURCE       .
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominini; Homo.
REFERENCE    1 (bases 1 to 1705)
AUTHORS      Li,W., Metzker,M.L., Caskey,C.T. and Petrukhin,K.
TITLE        Human retinal-specific delta 6 fatty acid desaturase
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 1705)
AUTHORS      Li,W., Metzker,M.L., Caskey,C.T. and Petrukhin,K.
TITLE        Direct Submission
JOURNAL      Submitted (11-MAR-1999) Human Genetics, Merck Research
              Laboratories, P.O. Box 4, West Point, PA 19486, USA
FEATURES
source       Location/Qualifiers
            1..1705
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /chromosome="11"
               /map="11q13"
            1..1705
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               /name="CYB5RP"
               /note="fatty acid desaturase; retina-specific"
               /codon_start=1
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               QDGPLNAQIVDEPRRALHOAEDMKTLFDSPEFEALIGHITAMVLMLLYLGPGMGLLAEESS
               VSALAALFLATISQAQSWCLQHDLDLHASIFRKSWMNHVAOKFYWGAKGFSAHMNNFR
               HQHNAAKPIFTFKDPRDYTAAPFLLGESSVEGRKKRYLPYNOQHLETFPIGPPLLT
               LVNEVENLAVMLVGMQWADLMAASFYAREFLSLPYGVGYLLFFVAVRVLESIM
               FVVIQDMHIIPKEIGHEKRDWVSOLAATVEPSLPTNMFSGLNFQIHHLFPRK
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BASE COUNT    324 a          560 c          480 g          341 t
ORIGIN
Query Match      20.9%   Score 125.4; DB 9; Length 1705;

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 8, 2002, 03:34:29 ; Search time 6458.34 Seconds
(without alignments)
1302.574 Million cell updates/sec

Title: US-09-806-088-1_COPY_18000_18401

Perfect score: 1 gattctgcaactgagctcct.....cattcagatgtattatgag 402

Sequence: 1 gattctgcaactgagctcct.....cattcagatgtattatgag 402

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008
Listing first 45 summaries

Database :

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2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
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29: em_vl:*
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33: em_hlg_inv:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Match Length DB ID Description

Result No.	Query Match Length DB ID	Description
1	402 100.0 112309	AC003025 Human Chr
2	402 100.0 142092	AF139813 Homo sapi
3	402 100.0 185035	AC004770 Homo sapi
4	402 100.0 196080	AC004228 Homo sapi
5	360.4 89.7 133683	AC084857 Homo sapi
6	343 85.3 1816	BC004901 Homo sapi
7	341.4 84.9 1705	AF134404 Homo sapi
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28	42.2 10.5 70621	AC068368 Homo sapi
29	42 10.4 77897	AF003333 Oryza sat
30	41.6 10.3 230741	AC087889 Mus muscu
31	41.6 10.2 122715	AC092558 Oryza sat
32	41 10.2 125020	AF429315 Homo sapi
33	40.8 10.1 177375	AC094559 Rattus no
34	40.8 10.1 177883	AC046159 Homo sapi
35	40.6 10.1 1335	AX253298 Sequence
36	40.6 10.1 2621	HSMB00210 Homo sapi
37	40.6 10.1 173773	AL645608 Homo sapi
38	40.6 10.1 210944	AL390719 Homo sapi
39	40.4 10.0 99281	AC110492 Homo sapi
40	40.4 10.0 168084	AC007037 Homo sapi
41	40.4 10.0 172516	AC091672 Papio cyn
42	40.4 10.0 185666	AC048389 Homo sapi
43	40.2 10.0 125571	AP003703 Oryza sat
44	40 10.0 1508	AF126798 Mus muscu
45	40 10.0 1546	AB021980 Rattus no

ALIGNMENTS

RESULT 1
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LOCUS Human Chromosome 1p12.2 PAC clone pDU466a11, complete sequence.
DEFINITION AC003025
ACCESSION AC003025
VERSION AC003025.1 GI:3537308
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 112309)
AUTHORS Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basil,M.,
Buetler,D., Bumeister,R., Card,P., desailloat,F., Dunn,J.,
English,C., Ehrldge,S., Garner,H.R., Gee,Y., Gordon,M., Gotway,G.,
Grant,O., Hahner,L., Joslin,J., Lewis,E., Loo,H., Loo,K.N.,
Major,T., McFarland,J., Newton,J., Osborne-Lawrence,S.,
Schageman,J., Schultz,R.A., Scimson,S., Syed,M., and Ward,T.
HTGS Submission
Unpublished
2 (bases 1 to 112309)
JOURNAL REFERENCE
AUTHORS Evans,G.A., Athanasiou,M., Bradbury,P., Brignac,S., Bumeister,R.,
Davis,C., English,C., Franklin,T.L., Garner,H.R., Gordon,M.,

Golway,G., Grant,O., Hahner,L., Harris,J., Hinson,S.,
 Narayanaswamy,U., Newton,J., O'Brien,K., Oliver,T., Patel,P.,
 Probst,S., Rayner,S., Schageman,J., Schilling,P., Schultz,R.,
 Syed,M., Valenzuela,D., Ward,T. and Wilson,R.
 Direct Submission
 Submitted (21-OCT-1997) Genome Science and Technology Center,
 University of Texas Southwestern Medical Center at Dallas, 5323
 Harry Hines Blvd, Dallas, TX 75235-8591, USA
 3 (bases 1 to 112309)
 Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M.,
 Buetler,J., Bumeister,R., Card,P., deSailboat,F., Dunn,J.,
 English,C., Elbridge,S., Garner,H.R., Gee,V., Gordon,M., Gotway,G.,
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 Major,T., McFarland,J., Newton,J., Lewis,E., Loo,H., Loo,K.N.,
 Schageman,J., Schultz,R.A., Stimson,S., Syed,M. and Ward,T.
 Direct Submission
 Submitted (23-JUL-1998) Genome Science & Technology Center,
 University of Texas Southwestern Medical Center, 5323 Harry Hines
 Blvd, Dallas, TX 75235-8591, USA
 On Jul 23, 1998 this sequence version replaced gl:2554967.
 IMPORTANT: This submission contains the entire insert of clone
 PDJ466a1. PDJ466a1 comes from a PAC library constructed at the
 Roswell Park Cancer Institute by the Pieter de Jong group. This
 clone has been finished according to strict quality criteria and
 attempts have been made to resolve all base calling problems such
 as compressions and repetitive elements. The expected Phred/Phrap
 calculated errors/10kb is 0.18. In addition, this sequence has
 been finished such that 99.9% of consensus base calls consist of
 either double-stranded coverage or 2 types of labeling chemistry on
 one strand.
 Further information regarding the map of this region or
 annotation of PDJ466a1 can be found at
<http://gestc.swmed.edu/chromosol.htm>.
 CHROMOSOMAL LOCUS: This PAC clone comes from the Chromosome
 11p12.2 Best's disease region mapped between STS D11S461 and EST
 A1NAK. This region spans over 1.5 Mbp.
 MARKER CONFIRMATION: EST: FTH (fertilin heavy chain mRNA)
 MAPPED CLONE OVERLAP: HTGS submitted PAC clones pdu519c13 and
 pdu756b9.

FEATURES
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Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 114009 CGGGAGAGAGAGGGCTCGAGGACCCAGCAACCAAGCCAGCCGGGGATGCAATACCC 114068

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pdu519013. pdu519013 comes from the RPCI-3 PAC library constructed
 at the Roswell Park Cancer Institute by the Pieter de Jong group.
 CHROMOSOMAL LOCUS: This PAC clone comes from the Chromosome
 11p12.2 Best's disease region mapped between STS D11S461 and EST
 AHNK. This region spans over 1.5 Mbp.
 MARKER CONFIRMATION: EST; FTH (ferritin heavy chain mRNA), STS
 D11S699 and WI-7524
 MAPPED CLONE OVERLAP: PACs pdu466a11 and pdu756b9.

FEATURES

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Best Local Similarity	100.0%;	Pred. No. 4.5e-102;		
Matches 402;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	gactctgcaactgaagctctcctaacaacacaccccaactgtgcaaccccaactcccaagtcctc	60
Db	102909	gattcttgcaacctgaagctccttaacacccaccccaactgtgcaaccccaactcccaagtcctc	102850
QY	61	gaagaagctctgctgacatcttgctggaagcgttacctccatcagtgaaggaacaaccagg	120
Db	102849	gaagaagctctggaagatcttggtgctggaagcgttacctccatcagtgaaggaacaaccagg	102790
QY	121	cgaggcagaagaagtggtccagggcacacgaacaaagccagcccccgcgggagatgataccc	180
Db	102789	cgggcagacgaagagggctcagagggcaccagacacacacaccccccgcgggagatgataccc	102730
QY	181	caaacacctcacaactcgcgcagccctcggggggtggccctctgcctcctcctctgttaactgtgtcttc	240
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QY	241	ccctcgcgcaccccccacacatgtgtatctcagaagccctatgaccttggctctcgtggccctgag	300
Db	102669	cccgcgcgcaccccccacacatgtgtatctcagaagccctatgaccttggctctcgtggccctgag	102610
QY	301	gaacagtgtagagagggaggtgagcatagcaaatcttccctagagcgagaaattggygggaag	360
Db	102609	gacacggcggtgagagggaggtgagcatagcacaattttcttaagacgagaaattggygggaag	102550
QY	361	ctgtatatttataatataaatacatctcaagatattatattggg	402
Db	102549	ctgtatatttataatataaatacatctcaagatattatattggg	102508

RESULT	5
LOCUS	AC0084857
DEFINITION	AC0084857 Homo sapiens chromosome 11, clone CTD-323J1N5 map 11, WORKING DRAFT
ACCESSION	AC0084857
VERSION	AC0084857.1
KEYWORDS	GI:11276215
SOURCE	HTG: HTGS_PHASE1; HTGS_DRAFT.
ORGANISM	human.
REFERENCE	Homo sapiens
ATTORNS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL	1 (bases 1 to 133683)
REFERENCE	1 (bases 1 to 133683)
ATTORNS	Barren, B., Linton, L., Nusbaum, C. and Lande, E.
TITLE	Homo sapiens chromosome 11, clone CTD-323J1N5
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 133683)
ATTORNS	Barren, B., Linton, L., Nusbaum, C., Lande, E., Abraham, H., Allen, N.,
TITLE	Anderson, S., Barna, N., Bastien, Y., Bede, F., Boguslavsky, L.,
JOURNAL	Boukigaliet, B., Brown, A., Burrell, G., Campopiano, A., Castle, A.,
REFERENCE	Choelel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
ATTORNS	Dezavallano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P.,
TITLE	Fitzellang, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M.,
JOURNAL	Graham, J., Grand-Pierre, N., Hagos, B., Heatford, A., Horton, L.,
REFERENCE	Iliev, I., Johnson, R., Jones, C., Kann, L., Kartas, A., Larocque, K.,
ATTORNS	Lamarates, R., Landers, T., Lehoczy, J., Levine, R., Liu, C., Liu, G.,
TITLE	Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKenna, K.,
JOURNAL	McPheters, R., Meldrum, J., Menes, L., Mihova, T., Mlenga, V.,

TITLE	Direct Submission
JOURNAL	Submitted (22-NOV-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02144, USA
COMMENT	All repeats were identified using RepeatMasker. 544,100 bp 22-Nov-2000

Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Ribbeck, M., Riley, R., Rougez, P., Rotman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Souquet, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (22-NOV-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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*	1460	1559:	gap of 100 bp	
*	1560	2520:	contig of 961 bp	in length
*	2621	2620:	gap of 100 bp	
*	2621	6338:	contig of 3714 bp	in length
*	6335	6434:	gap of 100 bp	
*	6435	11913:	contig of 5479 bp	in length
*	11914	12013:	gap of 100 bp	
*	12014	20755:	contig of 8743 bp	in length
*	20757	20856:	gap of 100 bp	
*	20857	28733:	contig of 8879 bp	in length
*	29756	29835:	gap of 100 bp	
*	29836	38645:	contig of 8810 bp	in length
*	38646	38745:	gap of 100 bp	
*	38746	52193:	contig of 13448 bp	in length
*	52194	52293:	gap of 100 bp	
*	52294	65209:	contig of 12916 bp	in length
*	65210	65309:	gap of 100 bp	
*	65310	79796:	contig of 14487 bp	in length
*	79797	79896:	gap of 100 bp	
*	79897	95896:	contig of 16000 bp	in length
*	95967	95996:	gap of 100 bp	
*	113440	113519:	contig of 17423 bp	in length
*	113440	113519:	gap of 100 bp	
*	113520	133683:	contig of 20164 bp	in length

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BASE COUNT 31520 a 34761 c 35336 g 30857 t 1209 others
ORIGIN

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Best Local Similarity 99.7%; Pred. No. 2.2e-90;
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 41 ccccccacccaggtccctgagaagctgtgacatctgtcgtgagcgtctacatccat 100
DB 52294 ccccccacccaggtccctgagaagctgtgacatctgtcgtgagcgtctacat 52353
QY 101 cagtgaggaagcaaccagagcgagagagagctcagagcaccagcaaccagcagc 160
DB 52354 cagtgaggaagcaaccagagcgagagagagctcagagcaccagcaaccagcagc 52413
QY 161 ccccgagggatcgatatacccccacccctccatctgagcagctggggtgcctgcctgc 220
DB 52414 ccccgagggatcgatatacccccacccctccatctgagcagctggggtgcctgcctgc 52473
QY 1221 ctctgtagctgttctctccctcgcgcccctcacatgtatattacagcagccctatgac 280
DB 52474 ctctgtagctgttctctccctcgcgcccctcacatgtatattacagcagccctatgac 52533
QY 281 ctgagctctgggctcgatgaggaagggatagaaggaaggtgagcatatgacatttcccta 340
DB 52534 ctgagctctgggctcgatgaggaagggatagaaggaaggtgagcatatgacatttcccta 52593
QY 341 gaagcgaagctggggaagagctgtattatataaataacatacattagattatagg 400
DB 52594 gaagcgaagctggggaagagctgtattatataaataacatacattagattatagg 52653
QY 401 ag 402
DB 52654 ag 52655

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RESULT 6
LOCUS BC004901 1816 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, fatty acid desaturase 3, clone MGC:4158
IMAGE:3532219, mRNA, complete cds.
ACCESSION BC004901
VERSION BC004901.1 GI:13436175

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KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1816)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabos-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbioology.org>
contact: amadansystemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Kettelman and Anuradha Madan

FEATURES
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Location/Qualifiers
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BASE COUNT 351 a 592 c 528 g 345 t
ORIGIN
Query Match      85.3%; Score 343; DB 9; Length 1816;
Best Local Similarity 100.0%; Pred. No. 9.6e-86;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 caggtccctgaagaagctctgtgacatctgctgtgagcctcctccatcagtgaaagca 111
DB 1446 CAGGTCCCTGAAGAAGCTGTGACATCTGGCGTGGACGCTTCACATCAGTGAAGCA 1505
QY 112 acaccagcgaggaagagctcagggcaaccagcaaccagcaaccgcccggcgagga 171
DB 1506 ACACCAGCGGAGGAGGAGGCTCAGGAGGACACACACACACACACGCCCCGGGGGA 1565
QY 172 tegtataccccaccctcagctgagcagcctgggggtgcctgctcctcctctgact 231
DB 1566 TCGATACCCACCCCTCCACTGCGCAGCGCTGGGGGGTGGCCCTGCTCCTGCTACT 1625
QY 232 gtgtctccctcggccctcacatgtgattcagagacccctatgacctgtgctc 291

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Db 1626 GTGCTCTCCCTCGGCCCCCTCACATGTGATTCACAGCCCTATGAGCTTGGCTCTGG 1685
Oy 292 gccatgtagcaggggtgaaggatgaatagatagacatttctctagaaggaatt 351
Db 1686 gccatgtagcaggggtgaaggatgaatagatagacatttctctagaaggaatt 1745
Oy 352 gggggaagcgtgtatttattatataaatacattcagatgta 394
Db 1746 GGGGGAAGCTGTATTATTATTAATAATACATTGAGATGA 1788
RESULT 7
AF134404 AF134404 1705 bp mRNA linear PRI 19-MAY-1999
LOCUS Homo sapiens delta-6 fatty acid desaturase (CYB5RP) mRNA, complete
DEFINITION cds.
ACCESSION AF134404 GI:4868365
VERSION AF134404.1
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1705)
AUTHORS Li, W., Metzker, M.L., Caskey, C.T. and Petrukhn, K.
TITLE Human retina-specific delta 6 fatty acid desaturase
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1705)
AUTHORS Li, W., Metzker, M.L., Caskey, C.T. and Petrukhn, K.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-1999) Human Genetics, Merck Research
Laboratories, P.O. Box 4, West Point, PA 19486, USA
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VPSALAPFLTAISOQDOSKCLQHDPLGHSIFKSNMNHVAKQVKNQGLGFSAHMNER
HFQHNAPNIFHKDPDVTVAAPVFLDESSVERGKKRRRLPYNQDHLFPLGLPPLT
LVNVEVENLAVMLQWADLMAASFYARFLSLPLFGVGVLLFVAARVLESHM
FWITQMNHLPKEIGHKRDWVSQLAATCWVPSLPLNMSGHILNFOIEHILFPRM
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BASE COUNT 324 a 560 c 480 g 341 t
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Best Local Similarity 99.7%; Pred. No. 2.7e-85;
Matches 342; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1474 TCGATACCCCAACCCCTCCACTGAGCCAGCTGGGGGTGACATGACCTGCTGCTACT 1533
Oy 292 gtgtcttcccttgcccccctcaatgtgtatttgagagccctatagcttgctcgg 291
Db 1534 GTTGCTTCCCTTGSCCCCTCACATGTATTCACAGCCCTATGAGCTTGGCTG 1593
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Db 1594 GCTGATGGGACAGGGGTAGAGGAAGGTGACATTCACATTTCTGAGCGAGAAAT 1653
Oy 352 gggggaagcgtgtatttattatataaatacattcagatgta 394
Db 1654 GGGGGAAGCTGTATTATTATTAATAATACATTGAGATGA 1696
RESULT 8
AX035942 AX035942 1757 bp DNA linear PAT 15-NOV-2000
LOCUS Sequence 3 from Patent EP1035207.
DEFINITION AX035942
ACCESSION AX035942
VERSION AX035942.1 GI:11191484
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1757)
AUTHORS Margardt, A. and Weber, B. H.
TITLE Cdn molecules of the members of gene family encoding human fatty
acid desaturases and their use in diagnosis and therapy
JOURNAL Patent: EP 1035207-A 3 13-SEP-2000;
MULTIGENE BIOTECH GMBH (DE)
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Oy 112 acaccagcgcggaaggaaggtctcagggcaccagcaacaaagccagcccgcgga 171
Db 1477 ACACCCAGCGCGGAGAGAGAGGGCTCAGGGCACACCAACCAAGCCAG-CGCCGGCGGA 1535
Oy 172 tcgataccccccccctcagctgagcagcctgagggtgctcctgctgctcctcctgact 231
Db 1536 TCGATACCCCAACCCCTCCACTGAGCCAGCTGGGGGTGCTGCTGCTGCTGCTGCTACT 1595
Oy 232 gtgtcttcccttgcccccctcaatgtgtatttgagagccctatagcttgctcgg 291
Db 1596 GTTGCTTCCCTTGSCCCCTCACATGTATTCACAGCCCTATGAGCTTGGCTG 1655
Oy 292 gccatgtagcaggggtgaaggatgaatagatagacatttctctagaaggaatt 351
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LOCUS Homo sapiens fatty acid desaturase 3 (FADS3) mRNA, complete cds.
DEFINITION

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ACCESSION AF084560.1 GI:10798852
VERSION AF084560.1
KEYWORDS
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1757)
AUTHORS Marquardt, A., Stohr, H., White, K. and Weber, B. H. F.
CDNA cloning, genomic structure, and chromosomal localization of
three members of the human fatty acid desaturase family
JOURNAL Genomics 66 (2), 175-183 (2000)
MEDLINE 20318619
PubMed 10860662
REFERENCE 2 (bases 1 to 1757)
AUTHORS Marquardt, A., Stohr, H., Passmore, L. A., Kraemer, F., Rivera, A. and
Weber, B. H. F.
Direct Submision
JOURNAL Submitted (05-AUG-1998) Institute of Human Genetics, University of
Muerzburg, Biozentrum, Am Hubland, Muerzburg D-97074, Germany
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BASE COUNT 318 a 580 c 517 g 342 t
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Query Match 82.1%; Score 330; DB %; Length 1757;
Best Local Similarity 99.7%; Pred. No. 4,4e-82;
Matches 341; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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OY 52 caagtcctcgaagaagtcgtgtgacatctgtgtgagcctactcactcgaagtaagca 111
|||||
DB 1417 CAGGTCCCTGTAAGAGTCTGTCATCTGGCTGACCCCTACCTCCATCTGTAAGCA 1476
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OY 112 acacccagggcgagcagaagggctcagagggcagcagcaaccaagcagcccgcgagga 171
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DB 1477 ACACCCAGGGCGGACAGAAAGGCTCAGGGCAGCAGCAACCAAGCGAG -CCCGCGCGGA 1535
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OY 172 tcgataccccaccctcactgagcagcctgagggtgacctgacctcctctctgtact 231
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DB 1536 TCATATCCCCACCCCTCCTGAGCCAGCTGCGGGGTGCTGCTGCTGCTCTCTGACT 1595
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OY 232 gttgtctccctcggcccccctacatgigtalttaagcagccctatgacctgtctg 291
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DB 1596 GTTGTCTTCCCTCGCGCCCTCACATGTCTATTGAGCAGCCCTATGCGCTGGCTCGG 1655
|||||
OY 292 gctcgtatggacaggggtagaaggaggtgagcatatgacatttcctcagggcagaatt 351
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DB 1656 GCTCGATGGACAGGGGTAGAGGAGGTGAGCATATGACATTTTCTTAGACGAGAAATT 1715
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OY 352 gggggaagcgtattattattataataaacattcagatgt 393
|||||
DB 1716 GCGGGAAGCGTATATTATTTATTAATAAATACATTCAGATGT 1757
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RESULT 10
AP000591 138627 bp DNA linear HTG 30-MAY-2000
LOCUS Homo sapiens chromosome 11 clone CMB9-22K5 map 11q13, WORKING DRAFT
DEFINITION
SEQUENCE, 28 unordered pieces.
ACCESSION AP000591.3 GI:8118797
VERSION AP000591
KEYWORDS HNG; HTGS PHASE1; HTGS DRAFT.
SOURCE Homo sapiens DNA, clone:CMB9-22K5.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 138627)
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Homo sapiens 138,627 genomic DNA of 11q13
JOURNAL Published only in Database (1999) In press
2 (bases 1 to 138627)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submision
TITLE Submitted (12-OCT-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitsato Univ., 1-15-1, Kitsato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hnp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
On May 31, 2000 this sequence version replaced gi:6997481.
COMMENT
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hnp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDrafl1
Center clone name: CMB9-22K5
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 122298 bases at least Q40
Consensus quality: 130648 bases at least Q30
Consensus quality: 134094 bases at least Q20
Insert size: 135927; sum-of-contigs
Quality coverage: 4.01x in Q20 bases; sum-of-contigs
-----
NOTE: This is a 'working draft' sequence. It currently consists of
28 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
1 20726 contig of 20726 bp in length
20827 34666 contig of 13840 bp in length
34767 46065 contig of 11299 bp in length
46166 53516 contig of 7351 bp in length
53617 61065 contig of 7445 bp in length
61166 67998 contig of 6833 bp in length
68099 74526 contig of 6428 bp in length

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74627 81299 contig of 6673 bp in length
81400 87316 contig of 5917 bp in length
87417 91541 contig of 4125 bp in length
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101229 104948 contig of 3720 bp in length
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126846 126945 gap of 100 bp

Sequence updated (20-Oct-1999)
Sequence updated (26-May-2000).
* NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

126946 129349: contig of 2404 bp in length
129350 129449: gap of 100 bp
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136177 136276: gap of 100 bp
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[illegible]

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AUTHORS	Osada, N., Kusuda, J., Tanuma, R., Ito, A., Hirata, M., Sugano, S. and Hashimoto, K.		
TITLE	Isolation of full-length cDNA clones from mouse brain cDNA library made by oligo-capping method .Unpublished (2000)		
JOURNAL	2 (bases 1 to 1818)		
REFERENCE	Hashimoto, K., Osada, N., Kusuda, J., and Sugano, S.		
AUTHORS			

Sequence updated (20-Oct-1999)	137519	136177	134132	133166	129450	128949	128667	125982	125665	125566	125565	125564	125563	125562	125561	125560	125559	125558	125557	125556	125555	125554	125553	125552	125551	125550	125549	125548	125547	125546	125545	125544	125543	125542	125541	125540	125539	125538	125537	125536	125535	125534	125533	125532	125531	125530	125529	125528	125527	125526	125525	125524	125523	125522	125521	125520	125519	125518	125517	125516	125515	125514	125513	125512	125511	125510	125509	125508	125507	125506	125505	125504	125503	125502	125501	125500	125499	125498	125497	125496	125495	125494	125493	125492	125491	125490	125489	125488	125487	125486	125485	125484	125483	125482	125481	125480	125479	125478	125477	125476	125475	125474	125473	125472	125471	125470	125469	125468	125467	125466	125465	125464	125463	125462	125461	125460	125459	125458	125457	125456	125455	125454	125453	125452	125451	125450	125449	125448	125447	125446	125445	125444	125443	125442	125441	125440	125439	125438	125437	125436	125435	125434	125433	125432	125431	125430	125429	125428	125427	125426	125425	125424	125423	125422	125421	125420	125419	125418	125417	125416	125415	125414	125413	125412	125411	125410	125409	125408	125407	125406	125405	125404	125403	125402	125401	125400	125399	125398	125397	125396	125395	125394	125393	125392	125391	125390	125389	125388	125387	125386	125385	125384	125383	125382	125381	125380	125379	125378	125377	125376	125375	125374	125373	125372	125371	125370	125369	125368	125367	125366	125365	125364	125363	125362	125361	125360	125359	125358	125357	125356	125355	125354	125353	125352	125351	125350	125349	125348	125347	125346	125345	125344	125343	125342	125341	125340	125339	125338	125337	125336	125335	125334	125333	125332	125331	125330	125329	125328	125327	125326	125325	125324	125323	125322	125321	125320	125319	125318	125317	125316	125315	125314	125313	125312	125311	125310	125309	125308	125307	125306	125305	125304	125303	125302	125301	125300	125299	125298	125297	125296	125295	125294	125293	125292	125291	125290	125289	125288	125287	125286	125285	125284	125283	125282	125281	125280	125279	125278	125277	125276	125275	125274	125273	125272	125271	125270	125269	125268	125267	125266	125265	125264	125263	125262	125261	125260	125259	125258	125257	125256	125255	125254	125253	125252	125251	125250	125249	125248	125247	125246	125245	125244	125243	125242	125241	125240	125239	125238	125237
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Sequence updated (26-May-2000).

* NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will

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Tue Oct 8 10:29:04 2002

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Page 18

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XX      Novel cytochrome b5-related protein useful for identifying modulators
XX      PT useful for treating retinal dysfunction such as macular degeneration,
XX      PT skin diseases, diabetic complications and cardiovascular disorders
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XX      Claim 2; Figure 2; 4app; English.
XX
XX      CYB5RP is a fatty acid desaturase and a cytochrome b5-related protein.
XX      CC Pharmaceutical compositions comprising an activator or an inhibitor of
XX      CC CYB5RP protein are useful for treating macular degeneration. The
XX      CC CYB5RP protein is useful for identifying its activators or inhibitors
XX      CC which are useful for treating abnormal conditions associated with
XX      CC CYB5RP protein activity such as skin disease, diabetic complications,
XX      CC inflammatory and autoimmune disorders, cardiovascular disorders and
XX      CC complications of viral infection. Large amounts of valuable essential
XX      CC fatty acids can be produced by the expression of CYB5RP protein.
XX
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DB      481 tccctcgggggtctgtcgcgacctcggccacgcgcttgaggtaccagaagctgtgtgac 540
QY      541 agcatggcgcgctcgaggagcgagggcgagggcgagggcgagggcgagggcgagggcgagggc 600
DB      541 agcatggcgcgctcgaggagcgagggcgagggcgagggcgagggcgagggcgagggcgagggc 600

```

```

RESULT 2
ID      AAH99727 standard; cDNA; 1772 BP.
XX
XX      AAH99727;
AC
XX
XX      16-OCT-2001 (first entry)
XX

```


CC CY5RP is a fatty acid desaturase and a cytochrome b5-related protein.
 CC Pharmaceutical compositions comprising an activator or an inhibitor of
 CC CY5RP protein are useful for treating macular degeneration. The
 CC CY5RP protein is useful for identifying its activators or inhibitors
 CC which are useful for treating abnormal conditions associated with
 CC CY5RP protein activity such as skin disease, diabetic complications,
 CC inflammatory and autoimmune disorders, cardiovascular disorders and
 CC complications of viral infection. Large amounts of valuable essential
 CC fatty acids can be produced by the expression of CY5RP protein.
 XX
 SO Sequence 1700 BP; 319 A; 560 C; 480 G; 341 T; 0 other:

Query Match 20.9%; Score 125.4; DB 21; Length 1700;
 Best Local Similarity 99.2%; Pred. No. 2e-12;
 Matches 126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 474 ctctgctccctcgaggtctgtctgacactcgccacccgctggtgacccagactcg 533
 |||||
 Db 1 ctctgctccctcgaggtctgtctgacactcgccacccgctggtgacccagactcg 60
 OY 534 tgcgtcagcatggcgcgctcgagagccggagacccggagacccgcagcg 593
 |||||
 Db 61 tgcgtcagcatggcgcgctcgagagccggagacccggagacccgcagcg 120
 OY 594 ggcgcgcg 600
 |||||
 Db 121 ggcacgcg 127

RESULT 6
 AAX53491
 AAX53491 standard; DNA; 114955 BP.

AAX53491;

05-JUL-1999 (first entry)

Human adenosine A1 receptor antisense oligonucleotide fragment.

XX Antisense oligonucleotide; multiple target; antisense treatment;
 XX impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.

Synthetic.

WO9913886-A1.

25-MAR-1999.

17-SEP-1998; 98WO-US19419.

09-JUN-1998; 98US-0093972.

17-SEP-1997; 97US-0059160.

(UYEC-) UNIV EAST CAROLINA.

NYCE JW;

WPI; 1999-229400/19.

New antisense oligonucleotides used in treatment of, e.g. pulmonary

vasoconstriction
 PT
 XX
 PS
 XX
 XX
 XX

CC The specification describes antisense oligonucleotides (AAX52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences AAX5272-74. These multiple target
 CC oligonucleotides (specifically AAX5180-211) can be used for the
 CC antisense treatment of diseases and conditions. Typical diseases and
 CC conditions are those associated with impaired respiration and
 CC inflammation, including lung diseases, pulmonary vasoconstriction,
 CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
 CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
 CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
 CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
 CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
 CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
 CC hepatic metastases, as well as all types of cancers which may metastasize
 CC or have metastasized to the lungs, including breast and prostate cancer.
 XX
 SO Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other:

Query Match 16.3%; Score 98; DB 20; Length 114955;
 Best Local Similarity 38.6%; Pred. No. 2.8e-08;
 Matches 225; Conservative 35; Mismatches 322; Indels 1; Gaps 1;

OY 19 cgcctccggtcccgagggcgctgagggcgagcccaacaggtcggtgt 78
 |||||
 Db 108310 cgcctbsnnndnngcgggcgcgccgctgctcctbsnnndnngcgggcgagc 108369
 OY 79 gtccccagggc-cgcgcgtccgggtgagtaagagccttggagacccggagaa 137
 |||||
 Db 108370 ggcgcctgctcgccsnnndnngcgggcgcgccgtgctcgccsnnndnngcg 108429
 OY 138 agggggcgagggagggcgcccgggcgagggcggtgtgctgctgtctcccgagag 197
 |||||
 Db 108430 gggcgagggcgctgctcgccsnnndnngcgggcgcgccgtgctcgccsnnndnng 108489
 OY 198 ggcggcgccctcgagccgctccctccctcgcccaatgagagaccccgcgctg 257
 |||||
 Db 108490 cggggcgcgccgctgctcgccsnnndnngcgggcgcgccgtgctcgccsnnndnngcg 108549
 OY 258 attggagcgagcgagggcgagccagccttggggcgggcgctggccgggggggg 317
 |||||
 Db 108550 gggggcgcgcgccgctggsnnndnngcgggggcgcgccctggsnnndnngcggggg 108609
 OY 318 ggcagggcgagcgagggcgcgccgctcgcggtataagggcgggagttccctcgcc 377
 |||||
 Db 108610 cggcgcgccctbsnnndnngcgggcgcgcccgccsnnndnngcgggcgcgccg 108669
 OY 378 ggcagcgcgagggcgagcgccgctcgctgagcgcgccggcgagggcgcgggg 437
 |||||
 Db 108670 snnndnngcgggggcgcgccggsnnndnngcgggggcgcgccsnnndnngcggggg 108729
 OY 438 cagcgggcgcgcgagggcgcgcccgggagcgcttcctccctcggggttgct 497
 |||||
 Db 108730 cggcggsnnndnngcgggcgcgccgsnnndnngcgggggcgcgccsnnndnngcggggg 108789
 OY 498 cggaacctcgccacccgctggtgatcccaagacatcgctgctgagcatggcgcgctgg 557
 |||||
 Db 108790 cgggsnnndnngcgggggcgcgccgctgctgctbaggcccsnnndnngcgggggcg 108849
 OY 558 ggaagcgagacggcgaggaaccccgagcgggggcgcgcg 600
 |||||
 Db 108850 gcgcgctgctcgccctbaggcccsnnndnngggggcgcg 108892

RESULT 7
 AAX02974/C
 ID AAX02974 standard; DNA; 3198 BP.
 XX
 XX
 XX
 XX

Db 133239 ccgaggagacgagccgaggagacgagccgaggagacgagccgaggagacgagcc 133298
QY 90 ccgagcctccgagtgatgacaaagccttgaaagccgagcccgagaaagggcgagac 149
Cc 133299 gggggagacgagccgaggagacgagccgaggagacgagccgaggagacgagcc 133358
QY 150 ggtgcccggagcagagctggcgagcagctgtctcccgaggagggcgagccgctc 209
Cc 133359 gggccgaggagacgagccgaggagacgagccgaggagacgagccgaggagac 133418
QY 210 gacgagccctccgagcagcagcagcagcagcagcagcagcagcagcagcagc 269
Cc 133419 ggggagcggggagcggagcggagcggagcggagcggagcggagcggagcgg 133478
QY 270 gcgagggtcagccagccttgaggcgagcccttgaggcgagcgaggcgagcagc 329
Cc 133479 agcggggagcagcggaggagcggaggagcggaggagcggaggagcggaggagc 133538
QY 330 gaggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 389
Cc 133539 ggggagcggggagcggaggagcggaggagcggaggagcggaggagcggaggag 133598
QY 390 ggcgacgctcgtcgtacgagcagcagcagcagcagcagcagcagcagcagc 435
Db 133599 cggggagcagcggaggagcggaggagcggaggagcggaggagcggaggagc 133644

RESULT 13
AAD25519/c
ID AAD25519 standard; DNA: 154746 BP.
XX
AC AAD25519;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human herpesvirus 2 complete DNA genome.
XX
KW Human herpesvirus 2; cytosolic; cancer; immunosuppressive; virucide;
KW antibacterial; fungicide; protozoacide; antitumoral; antiinflammatory;
KW antiarthritic; rheumatoid arthritis; neuroprotective; multiple sclerosis;
KW immune response; vasotropic; vaccine; gene therapy; autoimmune disease;
KW vasculitis; ds.
XX
KW Human herpesvirus 2.
OS
XX
PM WO200176643-A1.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-US11372.
XX
PR 07-APR-2000; 2000US-195680P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Orson FM, Kinsey BM, Bhogal BS;
XX
DR WPI: 2002-066308/09.
XX
PT Composition for oral delivery of vaccines, comprises expression vector
PT containing antigenic genomic sequence, bound to aggregated
PT protein-polycationic polymer conjugate or suspension
XX
PS Disclosure; Page 90-132; 145pp; English.
XX
CC The invention relates to a composition comprising an expression vector
CC bound to an aggregated protein-polycationic polymer conjugate or
CC suspension. The expression vector contains a promoter polynucleotide
CC sequence operatively linked to a polynucleotide sequence encoding an
CC antigen which is a fragment of a gene or genome associated with an
CC infectious disease, cancer and autoimmune disease such as rheumatoid
CC arthritis, vasculitis, and multiple sclerosis, pathogenic genomes
CC consisting of bacterium, fungus, protozoa and virus such as human

Cc immunodeficiency virus (HIV), herpes simplex virus (HSV), hepatitis C
Cc virus (HCV), influenza and respiratory syncytial virus (RSV), and
Cc optionally comprising a nucleotide sequence encoding a cytokine (or a
Cc cytokine expression vector), is useful for inducing an immune response
Cc (systemic and/or mucosal) in an organism. The cytokine expression vector
Cc contains a sequence for granulocyte macrophage-colony stimulating factor
Cc (GM-CSF) or interleukin-12 (IL-12). The polynucleotide sequences encoding
Cc the antigen and the cytokine are under transcriptional control of same or
Cc different promoter polynucleotide sequences. The expression vector, as a
Cc DNA vaccine is useful for treating a condition in an organism. The
Cc present sequence is human herpesvirus 2 complete DNA genome related
Cc to the invention.
XX
SQ Sequence 154746 BP; 23003 A; 54218 C; 54701 G; 22824 T; 0 other:

Query Match 11.9%; Score 71.6; DB 24; Length 154746;
Best Local Similarity 48.5%; Pred. No. 0.00049;
Matches 197; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

QY 30 cccgagggctgtgagcagcgtcgcgagcagcccaacaggtgctgtgtcccaagcc 89
Db 148503 CCGGGGGACCGGGGGGAGACGGGGGAGACGGGGGAGACGGGGGAGACGGGGC 148444
QY 90 ccgagcctccgagtgatgacaaagccttgaaagccgagcccgagaaagggcgagac 149
Db 148443 GGGGGGACGGGGGAGACGGGGGAGACGGGGGAGACGGGGGAGACGGGGGAGAC 148384
QY 150 ggtgcccggagcagagctggcgagcagctgtctcccgaggagggcgagccgctc 209
Db 148383 GGGCCGGGGGAGACGGGGGAGACGGGGGAGACGGGGGAGACGGGGGAGACGG 148324
QY 210 gacgagcctccgagtgatgacaaagccttgaaagcccgagcccgagtgaggagcagc 269
Db 148323 GGGGACGGGGGAGACGGGGGAGACGGGGGAGACGGGGGAGACGGGGGAGACGG 148264
QY 270 gcgagggtcagccagccttgaggcgagcccttgaggcgagcgaggcgagcagcagc 329
Db 148263 ACGGGGAGACGGGGGAGACGGGGGAGACGGGGGAGACGGGGGAGACGGGGGAG 148204
QY 330 gaggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 389
Db 148203 GGGGAGCGGGGAGACGGGGGAGACGGGGGAGACGGGGGAGACGGGGGAGACGG 148144
QY 390 ggcgacgctcgtcgtacgagcagcagcagcagcagcagcagcagcagcagc 435
Db 148143 CGGGGGAGCGGGGAGACGGGGGAGACGGGGGAGACGGGGGAGACGGGGGAGCG 148098

RESULT 14
AAS41761
ID AAS41761 standard; DNA: 31169 BP.
XX
AC AAS41761;
XX
DT 17-DEC-2001 (first entry)
XX
DE Genomic sequence #77 encoding novel human enzyme polypeptide.
XX
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW anti arthritic; nephrotropic; anticoagulant; ds.
XX
XX Homo sapiens.
OS
XX
PM WO200155301-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01239.

XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205513.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226888.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0231415.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0233397.
PR 14-SEP-2000; 2000US-0233398.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0233401.
PR 14-SEP-2000; 2000US-0233401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.

PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
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PR 08-NOV-2000; 2000US-0246532.
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PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
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PR 17-NOV-2000; 2000US-0249213.
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PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249266.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-02516719.
PR 06-DEC-2000; 2000US-0251679.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0255678.

PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI, 2001-465566/50.
XX
XX Novel polypeptides and polynucleotides useful for diagnosing,
PT preventing, treating neural, immune system, muscular, reproductive,


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PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
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PR 27-SEP-2000; 2000US-0235834.
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PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236570.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241321.
PR 20-OCT-2000; 2000US-0241785.
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PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249329.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250191.
PR 03-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.

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PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251889.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259676.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX
PS Disclosure: SEQ ID NO 30003; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
XX Sequence 31169 BP; 7807 A; 7136 C; 7464 G; 8761 T; 1 other;
SQ
Query Match 11.9%; Score 71.2; DB 22; Length 31169;
Best Local Similarity 47.8%; Pred. No. 0.00074;
Matches 240; Conservative 0; Mismatches 236; Indels 4; Gaps 1;
QY 81 ccccaagcccgctcgcgtgagtcgaagccttggaagccggaagcccggaagag 140
||| | |||| | | | | | | | | | | | | | | |
DB 322 ccccgacttgcgcttcgcgtgagtcggtggtggtggtggtggtggtggtggtggt 381
||| | | | | | | | | | | | | | | |
QY 141 gggcgagcagtgcccgagcagtggtggtggtggtggtggtggtggtggtggtggt 200
||| | | | | | | | | | | | | | | |
DB 382 gggcgagcagtgcccgagcagtggtggtggtggtggtggtggtggtggtggtggt 441
||| | | | | | | | | | | | | | | |
QY 201 ggcgctcgaagcgcgccttccttcgtgagcgaatggaacgaagcccgctgatt 260
||| | | | | | | | | | | | | | | |
DB 442 gggctcaggggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 501
||| | | | | | | | | | | | | | | |
QY 261 ggaagcgaagcgggtgagcagccttggtggtggtggtggtggtggtggtggtggtggt 320
|| | | | | | | | | | | | | | | | |
DB 502 ggggtcgggtcgcgttcgtggtggtggtggtggtggtggtggtggtggtggtggtggt 561
||| | | | | | | | | | | | | | | |
QY 321 aggcgaagcgaagcgggtggtggtggtggtggtggtggtggtggtggtggtggtggt 380
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DB 562 aggcgggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 617
||| | | | | | | | | | | | | | | |
QY 381 agcgggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 440
||| | | | | | | | | | | | | | | |
DB 618 cagcgggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 677
||| | | | | | | | | | | | | | | |
QY 441 cgggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcgg 500
||| | | | | | | | | | | | | | | |
DB 678 gggcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 737
||| | | | | | | | | | | | | | | |

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 8, 2002, 00:11:49 ; Search time 4866.45 Seconds
(without alignments)
1664.082 Million cell updates/sec

Title: US-09-806-088-1_COPY_1_600
Perfect score: 600
Sequence: 1 gctacagaccgggactcgg.....ccgcgacgcggggcgccg 600

Scoring table: IDENTITY_NUC
Gapop 10.0 / Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_estbhm:*
3: em_estlin:*
4: em_estmu:*
5: em_estcov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	219.4	36.6	300	9	AU100325 AU100325
2	209.4	34.9	583	10	BG826719 BG826719
3	209.4	34.9	1107	10	BG826581 BG826581
4	197.4	32.9	814	10	B1114230 B1114230
5	190.4	31.7	406	9	A1682885 A1682885
6	190.4	31.7	465	9	A1394672 A1394672
7	189.4	31.6	680	10	BE296427 BE296427
8	185	30.8	808	10	BG758416 BG758416
9	183	30.5	530	10	BE676674 BE676674
10	182.4	30.4	1013	10	BG828321 BG828321
11	179.8	30.0	444	9	AM138079 AM138079
12	179.4	29.9	409	12	AO937145 AO937145
13	167.6	27.9	471	9	AM087792 AM087792
14	163	27.2	737	10	BG829384 BG829384
15	159	26.5	962	9	AL537980 AL537980
16	155.4	25.9	850	10	BG753633 BG753633
17	153	25.5	483	10	BF732840 BF732840

18	144.4	24.1	849	10	B1254370
19	143.8	24.0	259	9	A1383926
20	143.2	23.9	499	9	A1806997
21	136.4	22.7	728	10	B1819067
22	133	22.2	299	9	A1493437
23	129	21.5	670	10	B1918614
24	112.4	18.7	810	10	B1837153
25	108.8	18.1	873	12	AG043471
26	105.6	17.6	1101	12	CNS0153F
27	105.4	17.6	841	12	AZ196416
28	105.4	17.6	878	10	BG786439
29	104	17.3	370	9	AA767321
30	103.2	17.2	685	10	BG786336
31	102.2	17.0	855	9	AL572700
32	102	16.9	153	9	AA765927
33	101.6	16.9	942	12	AG120142
34	101.2	16.9	724	12	AG171201
35	101	16.8	1005	10	B1824783
36	100.6	16.8	776	12	AG130889
37	100.2	16.7	922	12	AG072035
38	100	16.7	1016	12	CNS031U9
39	99.8	16.6	935	12	CNS005XK
40	99.2	16.5	908	12	CNS006B4
41	99.2	16.5	1101	12	CNS01523
42	99	16.5	1203	12	CNS015Y4
43	98.2	16.4	698	12	AZ184604
44	98.2	16.4	797	12	AG030595
45	97.8	16.3	776	12	CNS010RY

ALIGNMENTS

RESULT 1
LOCUS AU100325 300 bp mRNA linear EST 05-Apr-2001
DEFINITION AU100325 Sugano Homo sapiens cDNA library Homo sapiens CDNA clone
adSE00775 similar to Homo sapiens delta-6 fatty acid desaturase
(CYB5RP) mRNA, mRNA sequence.

ACCESSION AU100325
VERSION AU100325
KEYWORDS AU100325.1 GI:13551454
SOURCE EST.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
'H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
'K., Suyama,A. and Sugano,S.

TITLE

In silico mapping of the 5'-ends of human mRNAs using full-length
enriched and 5'-end enriched cDNA libraries constructed by

Oligo-capping method

JOURNAL

Unpublished (2001)
Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
Email: yusuzuki@ems.u-tokyo.ac.jp

FEATURES

location/Qualifiers
1..300
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="adSE00775"
/clone_lib="Sugano Homo sapiens cDNA library"

BASE COUNT 34 a /c 107 c 126 g 33 t
ORIGIN

Query Match 36.6%; Score 219.4; DB 9; Length 300;

REFERENCE	Mammalia, Eutheria: Primates, Catarrhini, Hominoidea, Homo. 1 (bases 1 to 808)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: WGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1CMI1698 row: k column: 03
 High quality sequence row: k column: 807.

FEATURES	Location/Qualifiers
source	1. .808

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4853114"
/clone_1bp="N1H.MGC.48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10b (phage-resistant)"
/note="organ: B-cells; Vector: pOT8; Site.1: XhoI;
Site.2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCGACGAG(5'). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a N1H.MGC library."

```

BASE COUNT	121 a	273 c	270 g	144 t
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ORIGIN

Query Match	30.8%;	Score 185;	DB 10;	Length 808;
Best Local Similarity	99.0%;	Pred. No. 1.4e-18;		
Matches 207; Conservative	0;	Mismatches 0;	Indels 2;	Gaps 2.

QY 392 gcaacgtctgctcgtacggcggccggcaggcgggcgagcagcggcgggcgc 45

Db 2 GCACGCTCGCTCGTACGCGCG-CCGCGCGCGCA-GGCGGCGCCGAGCAAGCGGCGCGCG 53

60 GGAGGCGGCGCGCGGAGCGCTTCGCTCCCTCGGGGTCTGCTCGGACCTCGGCCAC 114

QY 512 cgccctggatcccacgactcgtgctgcacatgagcgagcgcggagccgc 57

Db 120 CGCCGTGGCATCCCCAGGACATCTGCGCTGCAGCATGGGGCGGCGTGGGGGAGCCCGGACCCC 1

Db 180 GGGAGGGACCCGGCAGCCGGGGGCGCG 208

RESULT 9

BE676674					
LOCUS					
BE676674	530 bp	mRNA	linear	EST 08-SE	
NCT CGAP CUII Homo sapiens cDNA clone IMAGE:329652					

similar to TR:O95864 O95864 DELTA-6 FATTY ACID DESATURASE.
;contains PTR5.t3 TAR1 TAR1 repetitive element ;, mRNA sequen

ACCESSION	BE676674
VERSION	BE676674.1
KEYWORDS	GI:10037215
EST.	

SOURCE	ORGANISM
human.	
Homo sapiens	
Chordata: Vertebrata: Euteleostomi: Metazoa	

REFERENCE
1 (bases 1 to 530) Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
National Cancer Institute
P.O. Box 98
Bethesda, Maryland 20892

Email: cgapbs.riemail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:

Seq primer: -40UP from Gibco
High quality sequence stop: 451.

[illegible]

80 a	178 c	189 g	83 t
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ORIGIN

Query Match	Score	DB	Length
30.5%	183	10	530

Matches	183;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	----	--------	----	------	----

[illegible]

478 gcttcctcgggtattgtctcgacctgggcacccgcctggatccacgacctgtgcg 537

Db 61 GCTTCCCTCGGGGTCTTGCTCGACCTCGGCGACCGCCTGSGATCCCGAGGACTGTGCG 120

538 tgcacgcatggcgcggtctcgcgagcgcggagcgcgagagggaccgcgcgcgcgcggggcg 39

QY 598 ccg 600

Db	181	CCG	183
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RESULT 10
00000001

LOCUS	BG828321	1013 bp	mRNA	linear	EST 22-MAY-200
DEFINITION	602753757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4906263 5',				

Accession
Version
BG828321.1
GI:14175908

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
REFERENCE 1 (bases 1 to 1013)
KEYWORDS

Unpublished (1999)

Tue Oct 8 10:29:09 2002

us-09-806-088-1_copy_1_600.rst

Page 9

[illegible]

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-406-030A-3

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Query Match	11.1%;	Score 66.6;	DB 4;	Length 4488;
Best Local Similarity	48.0%;	Pred. No. 0.00034;		
Matches 280;	Conservative 1;	Mismatches 296;	Indels 6;	Gaps 3;

[illegible]

RESULT 5
US-08-483-533-39/c
; Sequence 39, Application US/08483533
; Patent No. 6172047
; GENERAL INFORMATION:
; APPLICANT: Roizman, Bernard
; APPLICANT: Chou, Joany
; TITLE OF INVENTION: Method for Treating Tumorigenic
; TITLE OF INVENTION: Diseases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,533
; FILING DATE: 07-MAR-95
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/419,853
; FILING DATE: 11-APR-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/861,233
; FILING DATE: 31-MAR-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, James P.
; REGISTRATION NUMBER: 28,491
; REFERENCE/DOCKET NUMBER: 28097/32742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1300 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-483-533-39

Query Match 10.8%; Score 65; DB 4; Length 1300;
Best Local Similarity 51.4%; Pred. No. 0.00073;
Matches 204; Conservative 0; Mismatches 185; Indels 8; Gaps 2;
QY 82 cccagagcccgagcgtcgtgagtcagagcctgagagccgagcccgaggaaggg 141
DB 725 ccgagccccaagcagcagctgagtcagagcctgagagccgagcccgaggaaggg 666
QY 142 ggcggagcagtgcccgagggagcagggctggt---ggcgccgctgtctcccgaggaagg 198
DB 665 ggcgtcgccggcggtcgccgggggtcgccgggggtcgccgggggtcgccgggggtcg 606
QY 199 ggcggcgccgtcgagcgcgcgcctcggtgagccaatgagagccgagcccgagc----- 253
DB 605 ccggggcgctccggcccccctcccgccgcccgcgcagcagccgagcccgagcagcagc 546
QY 254 cctgagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 313
DB 545 ctgcggtgacgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 486
QY 314 ggcggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 373

DB 485 GGTGGAGGGGTCAAGCCCGCCCTGAGGCCCGCGGCGGTGGGGGGGGGGGGGGGGGG 426
QY 374 cgcgcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 433
DB 425 GCGGTGGGGCGGCGCTGTGAGCGCGGCTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 366
QY 434 ggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 470
DB 365 ATGTGTGTGTGAGCGGAGCTCGGAACTGGAGC 329

RESULT 6
US-09-283-471A-39/c
; Sequence 39, Application US/09283471A
; Patent No. 6340673
; GENERAL INFORMATION:
; APPLICANT: Roizman, Bernard
; APPLICANT: Chou, Joany
; TITLE OF INVENTION: Method for Treating Tumorigenic Diseases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/283,471A
; FILING DATE: 04-APR-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/861,233
; FILING DATE: 31-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/419,853
; FILING DATE: 11-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/483,533
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, James P.
; REGISTRATION NUMBER: 28,491
; REFERENCE/DOCKET NUMBER: 27373/32742A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1300 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-283-471A-39

Query Match 10.8%; Score 65; DB 4; Length 1300;
Best Local Similarity 51.4%; Pred. No. 0.00073;
Matches 204; Conservative 0; Mismatches 185; Indels 8; Gaps 2;
QY 82 cccagagcccgagcgtcgtgagtcagagcctgagagccgagcccgaggaaggg 141
DB 725 ccgagccccaagcagcagctgagtcagagcctgagagccgagcccgaggaaggg 666
QY 142 ggcggagcagtgcccgagggagcagggctggt---ggcgccgctgtctcccgaggaagg 198


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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318, 837
FILING DATE: 13-OCT-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 93/01022
FILING DATE: 28-APR-1993
PRIOR APPLICATION DATA: 92.401.231.3
APPLICATION NUMBER: 92.401.231.3
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2150 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA(genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
TISSUE TYPE: Spleen tissue from healthy human
FEATURE:
NAME/KEY: CDS
LOCATION: 1810..1982
FEATURE:
NAME/KEY: misc_feature
LOCATION: 543
OTHER INFORMATION: C may be present or absent
FEATURE:
NAME/KEY: intron
LOCATION: 1980..2150
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..1809
US-08-318-837-1

Query Match 10.3%; Score 62; DB 2; Length 2150;
Best Local Similarity 48.28; Pred. No. 0.0023;
Matches 238; Conservative 0; Mismatches 250; Indels 6; Gaps 2;

QY 72 gtgtgtgttcccccagcccgctcgcgtgtgagtcagaagccttgaaagccgcaagcc 131
DB 1459 GTCGTGGCGCTGCGCGGGCGCGCGCGGAGACTTCCGCGCGCGCGCGCGCGG 1518
QY 112 gggaaaagggggcgagcgctgcccggcgagggcttggtgtggtggcgccgctgtcccg 191
DB 1519 GCGGGGCTGCGGGGCGGGGCGGGGCGGTGGGCGCCACCCCGGCTGAGCCCGCG 1578
QY 112 ggaaggggcgggcgccgctcgaagcgccctcccttgcgagcgaatgaaagcgaagccggc 251
DB 1579 GCGGACTCGGACTCGGCACTTCAGAGGCTCGGCGGCGCGCGCGCGGAGGCTCTGC 1638
QY 252 gcttgattgagagcgagcggtgcaagcgaagccttggtggcgcggtgctggcgggg 311
DB 1639 GCGCGGCTCCACGCGGCGCGGATGGGCGGCGCGCGCGCGCGGAGCACGCGGCGCGCG 1698
QY 312 cgggggggagcagcgagggcgagggcgccgctcggcgaggggtataagcggggaattccc 371
DB 1699 ACGTAGCCACCCGAGCTGAAAGCCCGCCCGCCCGCGCGCTCGCGGCTCCCGGGTTC 1758
QY 372 tgcgcgcgcagcgcggagggcgagcgcctgcctgtaagcgcgcgcgagcgagggcgggg 431
DB 1759 TCGCTCCGGGGTCTC-----GCGGACCGCGGGCGCGGGCGGAGGCGCGGCGCAGAGCATGC 1813
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QY 432 ccgagacagcgagcgcgagcgagcgcccgagagcgtcttcgcttcctccggagt 491
DB 1814 GGGCGCGCGCGCGCGCGCGCGCTGCGGCGCGCGCGGACGCTGCGCGGACCCCGCC 1873
QY 492 cttgctcg-gacctggccacagcgttgatcccaagactcgtgtgtgagcacttggcg 550
DB 1874 CCGGCGCGCGCGCGCGCGCGCTCCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1933
QY 551 ggttcggggagcg 564
DB 1934 GCGCGCGCGCGCGCAG 1947

RESULT 10
US-09-165-264-13
Sequence 13, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamorthy, Thuralayah
TITLE OF INVENTION: Multi-Local Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 320
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-13

Query Match 10.3%; Score 61.8; DB 4; Length 320;
Best Local Similarity 49.8%; Pred. No. 0.003;
Matches 156; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 158 ggggagggctgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 217
DB 2 ggggggggggggggggggggggggggggggggggggggggggggggggggggggggggggg 61
QY 218 cctccctggcgccaatgagacgagcgcccgctgattgagcgagcgagcgaggt 277
DB 62 ggggggggggggggggggggggggggggggggggggggggggggggggggggggggggggg 121
QY 278 cagcgaagccttggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 337
DB 122 ggggggggggggggggggggggggggggggggggggggggggggggggggggggggggggg 181
QY 338 cgcgcgtcgcggtataagc-cgggagttccctcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 397
DB 182 ggggggggggggggggggggggggggggggggggggggggggggggggggggggggggggg 241
QY 398 tcgtctgtaagcgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 457
DB 242 ggggggggggggggggggggggggggggggggggggggggggggggggggggggggggggg 301
QY 458 ggcgcgcggagc 470
DB 302 cgtgacgagggc 314

RESULT 11
US-09-165-264-7
Sequence 7, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamorthy, Thuralayah
TITLE OF INVENTION: Multi-Local Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
```



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; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-7
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Query Match          10.1%; Score 61.6; DB 4; Length 320;
Best Local Similarity 50.3%; Pred. No. 0.0032;
Matches 151; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
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QY 158 gggcagaggtgtggcgccgctgtccctccgagagggcgccgctcagcagcgc 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5 ggggggggggggggggggggggggggggggggggggggggggggggggggggg 64
QY 218 cctccctggcgccaatgagacgcagcccgccgctgattggagcggcgaggt 277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 65 ggggggggggggggggggggggggggggggggggggggggggggggggggggg 124
QY 278 cagccagccttggggcgccgctgtccgcgggcgggcgagggcgagggcgagg 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 125 ggggggggggggggggggggggggggggggggggggggggggggggggggggg 184
QY 338 cgcgcgcgcgcggtataagcgcgagagtccttcgcccgcgcgcgcgcgcgcgc 397
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 185 ggggggggggggggggggggggggggggggggggggggggggggggggggggg 244
QY 398 tcgctcgtacggcgccgagcgagcgagggcgagcgagcagcgagcgagcgagc 457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 245 ggggggggggggggggggggggggggggggggggggggggggggggggggggg 304
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RESULT 12

```
US-09-165-264-12
; Sequence 12, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vinayagamorthy, Thuralayah
; TITLE OF INVENTION: Multi-Loci Genomic Analysis
; FILE REFERENCE: 44/747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-12
```

```
Query Match          10.1%; Score 60.6; DB 4; Length 318;
Best Local Similarity 49.5%; Pred. No. 0.0048;
Matches 156; Conservative 0; Mismatches 159; Indels 0; Gaps 0;
```

```
QY 158 gggcagaggtgtggcgccgctgtccctccgagagggcgccgctcagcagcgc 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 ggggggggggggggggggggggggggggggggggggggggggggggggggggg 62
QY 218 cctccctggcgccaatgagacgcagcccgccgctgattggagcggcgaggt 277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 ggggggggggggggggggggggggggggggggggggggggggggggggggggg 122
QY 278 cagccagccttggggcgccgctgtccgcgggcgggcgagggcgagggcgaggg 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 ggggggggggggggggggggggggggggggggggggggggggggggggggggg 182
```

```
QY 338 cgcgcgcgcgcggtataagcgcgagagtccttcgcccgcgcgcgcgcgcgcgc 397
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Db 183 ggggggggggggggggggggggggggggggggggggggggggggggggggggg 242
QY 398 tcgctcgtacggcgccgagcgagcgagggcgagcgagcgagcgagcgagcgagc 457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 243 ggggggggggggggggggggggggggggggggggggggggggggggggggggg 302
QY 458 ggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 472
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 303 ggtgtgtgtgaagccc 317
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RESULT 13

```
US-09-165-264-11
; Sequence 11, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vinayagamorthy, Thuralayah
; TITLE OF INVENTION: Multi-Loci Genomic Analysis
; FILE REFERENCE: 44/747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-11
```

```
Query Match          10.1%; Score 60.4; DB 4; Length 320;
Best Local Similarity 50.0%; Pred. No. 0.0052;
Matches 151; Conservative 0; Mismatches 151; Indels 0; Gaps 0;
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QY 159 gggcagaggtgtggcgccgctgtccctccgagagggcgccgctcagcagcgc 218
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ggggggggggggggggggggggggggggggggggggggggggggggggggggg 60
QY 219 cctccctggcgccaatgagacgcagcccgccgctgattggagcggcgaggt 278
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 ggggggggggggggggggggggggggggggggggggggggggggggggggggg 120
QY 279 agccagccttggggcgccgctgtccgcgggcgggcgagggcgagggcgagggc 338
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 ggggggggggggggggggggggggggggggggggggggggggggggggggggg 180
QY 339 gccgcgcgcgcggtataagcgcgagagtccttcgcccgcgcgcgcgcgcgcgc 398
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Db 181 ggggggggggggggggggggggggggggggggggggggggggggggggggggg 240
QY 399 cgcctcgtacggcgccgagcgagcgagggcgagggcgagggcgagggcgaggg 458
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 459 gc 460
    ||
Db 301 gc 302
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RESULT 14

```
US-09-613-182-5/C
; Sequence 5, Application US/09613182
; Patent No. 6294653
; GENERAL INFORMATION:
; APPLICANT: Mayfield, Stephen
; TITLE OF INVENTION: RNA BINDING PROTEIN AND BINDING SITE USEFUL FOR
; TITLE OF INVENTION: EXPRESSION OF RECOMBINANT MOLECULES
; FILE REFERENCE: SCR21775
; CURRENT APPLICATION NUMBER: US/09/613,182
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```

1 CURRENT FILING DATE: 2000-07-10
2 PRIOR APPLICATION NUMBER: 09/341,550
3 PRIOR FILING DATE: 1999-07-13
4 PRIOR APPLICATION NUMBER: PCT/US98/0
5 PRIOR FILING DATE: 1998-01-16
6 PRIOR APPLICATION NUMBER: 60/035,955
7 PRIOR FILING DATE: 1997-01-17
8 PRIOR APPLICATION NUMBER: 60/069,400
9 PRIOR FILING DATE: 1997-12-12
10 NUMBER OF SEQ. ID NOS.: 14
11 SOFTWARE: PatentIn Ver. 2.1
12 SEQ. ID NO. 5
13
14 LENGTH: 2846
15
16 TYPE: DNA
17
18 ORGANISM: Chlamydomonas reinhardtii
19
20 FEATURE:
21
22 NAME/KEY: CDS
23 LOCATION: (19)..(2065)
24
25 OS-09-613-182-5

```

Query Match	10.18;	Score 60.4;	DB 4;	length 2846;
Best Local Similarity	47.58;	Pred. No. 0.0041;		
Matches 210; Conservative	0;	Mismatches 231;	Indels 1;	Gaps 1,

QY	160	gagcagcctctggtgtggtcgccgcgcgtgtctctccgcggaaggggcgcgcctcagacgcgcgc	219
Db	1924	GCACGACAGGTGCGGGGTCGACGTCGCCGCACTGCGGGGTACAGGCGCTCGCCGATCATCAT	18655
QY	220	tcctctgctgagccaaatgagacagagccgcgcgcgtgattgtgaaacggaacgcgggtgtca	279
Db	1864	CTTCTGCTGCTCGCGGCGCGGCGGCGGCGGCGGCGGCGGAGCGGATCAAGCGCTGCTGTGGGCGGC	18050
QY	280	gcaacagccttggtgggggcgcggggc -ctggccaggggcgcggggggggaagcgagagcgagcc	338
Db	1804	GGGGGGCTCCGGCTTCGGCCCGCGGCGGCAAGCGCCGCGGCGAGGGGGGCGCGCGCGGGG	17454
QY	339	gcccgtccgcgcggttataaagcggggagttccctctgcgcgcgcgcgcgcgcgcgcgcgcgc	398
Db	1744	CGCGCGGCGCGGCTCAAGCGGCGGCGCTTGGGCTGCTGGGCGAGGGGCGTTGTTGCCGCGGCC	16855
QY	399	cgctctgtctagc	458
Db	1684	CTGAGCGCGGCGGAGAGGGCGCGCGCGCGCACGGCGCGCCCGGGGCGCATAGGGGGGCGC	16255
QY	459	ggcgccggggagcgctcttcgccttcctcggtgtctgtctcgcgcgcgcgcgcgcgcgcgcgcgc	518
Db	1624	CATCATAGGGGCGCACCATCATCTCGGGGCGGCAATAGGGGCGCGCGGGGCGCGGCGCGG	15055
QY	519	gattcccaagactctgtcgtcagcaatgggcgcgcgtctcgggaagccgcgcgcgcgcgcgcgcgcgc	578
Db	1564	GCCAGGCGATCCCGCGGCGGCGCATCATAGCGGATGAGCGGATCATCATGATGCGCGGAGCGCGGCGCC	15055
QY	579	accgc	600
Db	1504	AGCAGCGATGCCGCGGGGCG 1483	

RESULT 15
US-08-483-533-37/c
Sequence 37, Application US/08483533
Patent No. 6172047
GENERAL INFORMATION:
APPLICANT: Rolzman, Bernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method for Treating Tumorigenic
TITLE OF INVENTION: Diseases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois

```

1  COUNTRY: United States of America
2  ZIP: 66066-6402
3
4  COMPUTER READABLE FORM:
5
6  MEDIUM TYPE: Floppy disk
7  COMPUTER: IBM PC compatible
8  OPERATING SYSTEM: PC-DOS/MS-DOS
9  SOFTWARE: Patentin Release #1.0, Version #1.25
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/08/483,533
12 FILING DATE: 07-MAR-95
13
14 CLASSIFICATION: 514
15
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: 08/419,853
18 FILING DATE: 11-APR-95
19
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: 07/861,233
22 FILING DATE: 31-MAR-92
23
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Zeller, James P.
26 REGISTRATION NUMBER: 28,491
27 REFERENCE/DOCKET NUMBER: 28097/32742
28
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 312/474-6300
31 TELEFAX: 312/474-0448
32
33 TELEX: 25-3856
34
35 INFORMATION FOR SEQ ID NO: 37:
36
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 1292 base pairs
39 TYPE: nucleic acid
40 STRANDEDNESS: single
41 TOPOLOGY: linear
42
43 MOLECULE TYPE: DNA (genomic)
44
45 US-08-483-533-37

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Query Match	9.98;	Score 59.4;	DB 4;	Length 1292;
Best Local Similarity	50.68;	Pred. No. 0.0066;		
Matches 198;	Conservative	0;	Mismatches 186;	Indels 7;
				Gaps 2;

QY	82	cccaagcccccgctctccggtgtgaggtcaagaagcctctgaagccgagccgagccgggaaagag	141
Db	725	ccgaagcccacagaccacagagatggcgcacaccgacgtggggcgagatcccgccg	666
QY	142	gacgagaaagctgcccccgaggagaggtctgagctgagcgcgctgtctcccgagagagtcg	201
Db	665	ggcttccgcgcgggtgcgcgggggtccgcggggggatccggggg-----tcgcgggggtccgg	612
QY	202	gcgcgcctcgaagccgcccctctgtagcgagccaatgagagaccgaagccccgcgcttgattg	261
Db	611	ggggcctccggcgcc--ccctcccccaccgcagcttcgcagagccagcccgccacagatgctcc	553
QY	262	gagcgagacgaggggtcaagcaagcctctgaggagccgtgagcgggtcctgacggggggggca	321
Db	552	gcggctgacccaccagccgagagggccagaccgagccggcagagagggccgcagagggggg	433
QY	322	gacgagagcgaagtcgagcgcgtccgcgcggttataaagtcgaggaagttccctgacgcgag	381
Db	492	tggcagggggtacagcccgcccccgcggccacacgcgcggcgttgaggggcccgggggcgccg	433
QY	382	gcgcgagagcgcacgcctcgtctgtaagtcgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	441
Db	432	ggcgcggcgagctgggcgcgcgcgcctcttgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	373
QY	442	gggagcgcgcgagagtcgagcccgagagtcgc	472
Db	372	cgctgcatacgtcgtcgtgcagccgagacac	342

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PN		WO200021557-A1.
XX		20-APR-2000.
XX		
XX	05-OCT-1999;	99WO-US23253.
XX	09-OCT-1998;	98US-0103760.
XX		
PA	(MERI) MERCK & CO INC.	
FI	Petrushkin K, Caskey CT;	
XX	WPI; 2000-317847/27.	

XX Novel cyclochrome b5-related protein useful for identifying modulators
PT useful for treating retinal dysfunction such as macular degeneration,
PT skin diseases, diabetic complications and cardiovascular disorders
XX
XX
PS Claim 2; Figure 2; 44pp; English.
PS
XX
XX Cyb5RP is a fatty acid desaturase and a cyclochrome b5-related protein
CC Pharmaceutical compositions comprising an activator or an inhibitor of
CC Cyb5RP protein are useful for treating macular degeneration. The
CC Cyb5RP protein is useful for identifying its activators or inhibitors
CC which are useful for treating abnormal conditions associated with
CC Cyb5RP protein activity such as skin disease, diabetic complications,
CC inflammatory and autoimmune disorders, cardiovascular disorders and
CC complications of viral infection. Large amounts of valuable essential
CC fatty acids can be produced by the expression of Cyb5RP protein.
XX
SQ Sequence 18402 BP; 3790 A; 5122 C; 5428 G; 4062 T; 0 other:

Query Match	100.0%;	Score 501;	DB 21;	Length 18402;
Best Local Similarity	100.0%;	Pred. No. 1.1e-142;		
Matches 501; Conservative	0;	Mismatches	0;	Gaps 0;

QY	1	aaaccgcgactctctacggaataatacaaaaattagcctggtgtggtgtgcttgacccctctaat	60
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QY	61	cccaacctactcaagatagatgaagtcagaagcacaagaatcctcttgaaaccttgagaggttgaggtttica	120
Db	9060	cccaacctactcaagatagatgaagtcagaagcacaagaatcctcttgaaaccttgagaggttgaggtttica	9119
QY	121	gtaaagccgagatcatgcccactgtcaacccagctctggtgagcaagagcaagaatctgtcttcaa	180
Db	9120	gtaaagccgagatcatgcccactgtcaacccagctctggtgagcaagagcaagaatctgtcttcaa	9179
QY	181	aaaaataaagaataataataaaaaatttagagagccaggtgtgtgtgcacacaacctgttaattctaac	240
Db	9180	aaaaataaagaataataataaaaaatttagagagccaggtgtgtgtgcacacaacctgttaattctaac	9239
QY	241	actttgagagagctgtgaagttgtagagatcgctgtgaagtcagagcaatttaagacatgacctagtc	300
Db	9240	actttgagagagctgtgaagttgtagagatcgctgtgaagtcagagcaatttaagacatgacctagtc	9299
QY	301	aacactagtagagactcttgacactcaacaaaaattccaagaatttaagaacatgtgtgtgacgt	360
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QY	361	tgcctgtagtcctacgtcgtcgtggtggtgagagctgtgaagtcagagatcaacattacgcacagaattt	420
Db	9360	tgcctgtagtcctacgtcgtcgtggtggtgagagctgtgaagtcagagatcaacattacgcacagaattt	9419
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QY	481	ctgtctcaaaaaaatttttca	501
Db	9480	ctgtctcaaaaaaatttttca	9500

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XX	
XX	
AC	AAC59917;
XX	
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DT	30-JAN-2001 (first entry)
XX	
XX	
DE	Human secreted protein cDNA sequence #11.
XX	
XX	
KW	Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX	antiallergic; hepatotrophic; antidiabetic; antiinflammatory; anticancer

KW		vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KM		cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
RN		neurological disease; infection; human; secreted protein; ss.
XX		
OS	Homo sapiens.	
XX		
PN	WO200055198-A1.	
XX		
PD	21-SEP-2000.	
XX		
PF	09-MAR-2000; 2000WO-US06012.	
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PR	12-MAR-1999; 99US-0124093.	
XX	23-NOV-1999; 99US-0166989.	
XX		
PA	{HUMA-} HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Ruben SM, Komatsoulis G;	
DR	WPI; 2000-587520/55.	
DR	P-PSDB; AAB28712.	
PT		
PT	Human secreted proteins and the nucleic acids that encode them, useful in gene therapy protocols and recombinant nucleic acid based procedures	
XX		
PS	Claim 1; Page 318; 391pp; English.	
XX		
CC	The invention relate to the isolation of genes AAC59907-C59956 encoding 50 human secreted proteins AAB28702-B28751. The genes can be used to generate fusion proteins by linking to the gene for the human immunoglobulin G Fc portion for increasing the stability of the fusion protein as compared to the human protein only. The genes and proteins are useful for preventing, ameliorating or treating medical conditions. e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, Rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.	
CC		
XX		
SQ	Sequence 1278 BP; 346 A; 262 C; 376 G; 289 T; 5 other;	
XX		
Query Match	85.2%; Score 427; DB 21; Length 1278;	
Best Local Similarity	92.7%; Pred. No. 1.5e-120;	
Matches 459; Conservative	0; Mismatches 35; Indels 1; Gaps 1	
OY	1 aaaccgcgacttaagaaatatacaaaaaattagctcggtgtgttgcttcacctaatt 60 	
Db	756 aaaccgcgactttaaagaatatatacaaaaattagctcggtgtgttgcttcacctaatt 815 	
OY	61 ccacacctactcagttagctgaagacaagaatctctttgaacctggagggttgaggttta 120 	
Db	816 ccacacctactcagttagctgaagacaagaatctctttgaacctggagggttgaggttta 875 	
OY	121 gtaaacgcgagatcatgccaatgcaaccccgcttgtggcgacagaagaagcttgttcaa 180 	
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OY	181 aaaataaaagataaatataaaaattagaagccaggtgtgtgccacacccgtactctcaac 240 	
Db	936 aaaataaaagataaatataaaaattagaagccaggtgtgtgccacacccgtactctcaac 995 	
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Db	996	acttgaggagcctgaagtgaggagatgcgttgtaagtcacgagcatttaagacatgcctaac	1055
Qy	301	aacatactgagaccttactactctacaacaaaatccaagaatlaatgagacatggtgcata	360
Db	1056	aacatactgagaccttactactctacaacaaaatccaagaatlaatgagacatggtgcata	1115
Qy	361	tgctctgaftcctactgcctgctcgtgggagcctgagtgaggagatcaactacgacagattt	420
Db	1116	cactgtactcaacagcactacagagagagctlaagtgaggatcacctgagcccggaagt	1175
Qy	421	caagctgcagctgagctgctgattatgcactgactccagcct-ggtgacagaatgagac	479
Db	1176	tgaagctgcagcagctgagcagatgtgcaccactgacctcctgctggcgcatacagcaaac	1235
Qy	480	cctgtctcaacaaa 494	
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XX	AA105510	standard; DNA; 17965 BP.	
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AC			
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DT	21-NOV-2001	(first entry)	
XX			
DE		Human reproductive system related antigen DNA SEQ ID NO: 8198.	
XX			
KM		Human; reproductive system related antigen; reproductive system disorder	
KW		cancer; gene therapy; ds.	
XX			
OS		Homo sapiens.	
XX			
PM		WO200155320-A2.	
XX			
PD	02-AUG-2001.		
XX			
PF	17-JAN-2001;	2001WO-US01339.	
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QY 421 caaggtcgacgtagctgtgattcgatccactgacccagcct-ggtgacagatgagc 479
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QY 480 cctgtctcaaaaaa 494
Db 7581 tccatctcaaaaaa 7595

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AA199172
ID AA199172 standard; DNA; 32134 BP.
AC AA199172;
XX
DT 07-JAN-2002 (first entry)
XX
DE Human excretory related polynucleotide SEQ ID NO 936.
XX
KW Human: neurotropic; neuroprotective; cytosolic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
KW antiparkinsonian; antistroke; antianaemic; antiarthritic; cancer;
KW antitumematic; hepatotropic; cerebroprotective; antiinflammatory;
KW antidiabetic; antidiabetic; antidiabetic; antidiabetic; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine;
KW excretory system; ds.
XX
OS Homo sapiens.
XX
PN W0200155313-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001MO-US01323.
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PR 31-JAN-2000; 2000US-0175065.
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RESULT 7
AAK69766
ID AAK69766 standard; DNA, 35115 BP.
XX
XX AAK69766;
AC
XX
DT 06-NOV-2001 (first entry)
DE
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24578.
XX Human immune/haematopoietic; immune/haematopoietic antigen; cancer;
KW Cytostatic; gene therapy; vaccine; metastasis; ds.
XX
XX Homo sapiens.
XX
XX W0200157182-A2.
XX
XX
XX 09-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US01354.
PF
XX
XX 31-JAN-2000; 2000US-0179065.
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Qy 478 gccctgtctcaaaaatttt 499
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Db 23297 accctgtctctcaaaaattt 23318

RESULT 9
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ID AAS26670 standard; DNA: 14176 BP.
XX
AC AAS26670;
XX
DE 07-NOV-2001 (first entry)
XX
DE Human genomic DNA encoding partial novel secreted protein, Seq ID 1644.
XX
KW Human; immunosuppressive; antiarthritic; ds; antirheumatic;
KW cytosolic; cardiant; vasotropic; cerebroprotective; nootropic;
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
KW vulnery; secreted protein; rheumatoid arthritis;
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW cerebrovascular disorder; cerebral ischemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;
KW corneal infection; wound healing; epithelial cell proliferation;
KW skin aging; food additive; preservative; antiproliferative.
XX
OS Homo sapiens.
XX
PN WO200155322-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001MO-US01341.
XX
XX 31-JAN-2000; 2000US-0179065.
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PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
PI	WPI; 2001-488783/53.	
XX		
PT	New nucleic acid molecules encoding 461 human secreted proteins for	
PT	diagnosing, preventing, treating or ameliorating medical conditions and	
PT	used as food additives or preservatives -	
XX		
XX		
PS	Disclosure; SEQ ID No 1644; 980bp; English.	
XX		
XX		
CC	The invention relates to isolated nucleic acid molecules and their	
CC	encoded secreted proteins. The nucleic acids and proteins are used to	
CC	prevent, treat or ameliorate a medical condition in e.g. humans, mice,	
CC	rabbits, goats, horses, cats, dogs, chickens or sheep. They	
CC	are also used in diagnosing a pathological condition or susceptibility	
CC	to a pathological condition. Antibodies to the proteins can also	
CC	be used in alleviating symptoms associated with the disorders and in	
CC	diagnostic immunoassays e.g. radioimmunoassays or enzyme linked	
CC	immunosorbent assays (ELISA). Disorders which are diagnosed or treated	
CC	include autoimmune diseases e.g. Rheumatoid arthritis,	
CC	hyperproliferative disorders e.g. neoplasms of the breast or liver,	
CC	cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders	
CC	e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.	
CC	Alzheimer's disease, infections caused by bacteria, viruses and fungi	
CC	and ocular disorders e.g. corneal infection, and many other	
CC	disorders listed in the specification. The polypeptides can also	
CC	be used to aid wound healing and epithelial cell proliferation, to	
CC	prevent skin aging due to sunburn, to maintain organs before	
CC	transplantation, for supporting cell culture of primary tissues, to	
CC	regenerate tissues and in chemotaxis. The polypeptides can also be used	
CC	as a food additive or preservative to increase or decrease storage	
CC	capabilities, fat content, lipid, protein, carbohydrate, vitamins,	
CC	minerals, cofactors and other nutritional components. The present	
CC	sequence is a genomic DNA encoding a partial novel secreted protein of	
CC	the invention.	

[illegible]

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CC	XX	PA	(HUMA-) HUMAN GENOME SCI INC.	
CC	XX	PI	Rosen CA, Barash SC, Ruben SM;	
CC	XX	DR	WPI; 2001-541565/60.	
CC	XX	PT	Nucleic acids encoding 3324 human nervous system antigen polypeptides,	
CC	XX	PT	useful for preventing, diagnosing and/or treating nervous system	
CC	XX	PT	cancers and metastases -	
CC	XX	PS	Disclosure; SEQ ID NO 12047; 1701pp + Sequence Listing; English.	
CC	XX	CC	The invention relates to novel genes (ABA11004-ABA21534) and proteins	
CC	XX	CC	(ABA1678-ABA1801) useful for preventing, treating or ameliorating	
CC	XX	CC	medical conditions e.g. by protein or gene therapy. The genes are	
CC	XX	CC	isolated from a range of human tissues disclosed in the specification.	

Db 25010 cgaagattgtccactgcacttgcacctgtgacagagtgcagattctgtctcaaaaaat 25068

RESULT 12
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ID AAI63523 standard; DNA; 32192 BP.
XX
AC AAI63523;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human kidney related polynucleotide SEQ ID NO 838.
KW Human; kidney antigen; immunosuppressive; antihypertic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW nootropic; neuroprotective; antibacterial; virucide; fungicide;
KW opthalmologic; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; anticancer; immune disorder; anticonvulsant; antiparasitic;
KW gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; ds.
XX
OS Homo sapiens.
XX
PN MO20015323-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01343.
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PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001.483426/52.
XX
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PI metastasis -
XX
XX
XX Disclosure; SEQ ID NO 21686; 3071pp + Sequence listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cystostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting

[illegible]

Db	568	AGAGGTGGCACTGATGCCAAGTACATGCCACTTCACCTCCAGCCTGGGACAAGACAA	647
Qy	481	ctgtctcaaaaaa	494
Locus	A0355178/c		
Definition	CITBI-El-2535L9.TF CITBI-El Homo sapiens genomic clone 2535L9, DNA sequence.	506 bp	Linear GSS 24-JAN-1999
Accession	A0355178		
Version	A0355178.1	GI:4182351	
Keywords	GSS.		
Organism Source	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C. Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building Unpublished (1997) Other GSSs: CITBI-El-2535L9.FR Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel.: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org End search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html . Seq primer: M13-21 Class: BAC ends.		
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Origin			
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Best Local Similarity	73.4%; Pred. No. 4, 5e-43;		
Matches	364; Conservative 0; Mismatches 123; Indels 9; Gaps 3		
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Db	506	AAAACCTCGCTTGATTAATAATACAAAAATTACTGGGTGTGTGGGGGCTGTAA	447
Qy	61	cacacctactcagttagtaagcacacaagatctctgaaccctggagggtgagttgca	120
Db	446	CCGAGTACTCTGGGAGAGCTGAGGCAGANAATCATCTGAACCACGAGGGGGAGTTCA	387
Qy	121	gtaacgcagatcatgtccaatgtcaaccagtcctggcggaagagcgcaagacttgttcaa	180
Db	386	GTGAGCTGAGATATGCGCATTCCTCACCTGGGCGACAGACGAGACTCTGTCAA	327
Qy	181	aaaataaagaataaataaataatlagaggccaggtgtgctcaacactgtlactcaac	240
Db	326	AAAAAGAAGAAAGAAAGAACCCAGGTAATGAC-----GGCTGTACTGTAAATTACAGA	274
Qy	241	actttggaggctgtaggtggaggagatgcgtttaagtaaggcaatttaagaatgcctcggc	300

Accession	Sequence	Position
D8	AAAGTTGGGAGGCCAAGTTGGAGGATCACTTGAGGGTAGGGTTCCGAGATTAACCTTGCGC	214
Q7	aacataatggaaccttgaacttacaataaaatcaaaa-cttaatgagacatgltgacat	359
D8	AACATGAGCAAGACCCGGGTCTACAAAACATTAAAAATGTTAACCGACGCACAGATGTT	154
Q7	gtgcctgtagttcctaagctgtcgtggaagcgtgaagltggagagatcaacttaagaccagatt	419
D8	GTGCCTGTAGTCTCAGCTACTCAGAGACACTGAGCAAGAGGATTGTCGGACCCCAAGG	94
Q7	tcaagcgtcagctgaagctgtgatctgacatgcactgcactcaacct-aggltgaagatgtagg	478
D8	TCAAGCGTCGCAATGAGCCATGCTTCTGCCACTGCACTCCAACTGGGAGACAAAGTAAGA	34
Q7	cctgtctcaaaaaa	494
D8	CCCTGTCTCTCAAAA	18

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OY	121	gttgccggaataatgcacatgcaaccgaacgttgggcaacagcaagactcgtctca	180
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OY	181	aaaaataaagataataaaaaaatatagagccaggtgtgtgtcacaacctgtactcaac	240
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Db	228	AAAAAATTTAAAAAATAAAAAATAAAATCA---CCGTAGCAACCTGTAAATTCAG	284
OY	241	actttggagagctgagatgtggagagatcgcttgaagtcacagcatlaagacatgcctaggc	300
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OY	361	tgcctgtagctcctagctgtctggggagctgaggttggagagatcaacttcagacagatt	420
	111		111
Db	405	CACCCGTAGTCCCAATTAATTGTGGGGGGCTGAAGCATGAGGTTCTCTGAGCCAGGAGT	464
OY	421	caagagctgacatgagctgtg-attgacatcactgcaatccagcct-ggtgacagatgtgagg	478
	111		111
Db	465	CAAAAGCTGCAGTAGCTGTGTATGTGCACACCTCACTCAACCTGGGGTGACAGAGTTAAG	524
OY	479	ccctgtctcaaaaaa	494
	111		111
Db	525	CCCTCTCTCAAAAAA	540

RESULT	12				
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DEFINITION	602372119F1 NTH_MGC_93 Homo sapiens cDNA clone IMAGE:4480109 5',				
ACCSSION	BG260565				
VERSION	BG260565.1				
KEYWORDS	EST.				
SOURCE	human.				

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1. (pages 1 to 948)
NIH-MGC. <http://mgc.nhl.nih.gov/>.
National Institutes of Health. Mammalian Gene Collection (MGC).
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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FEATURES
source
    cdna library preparation: life technologies, inc.
    cdna library arrayed by: the i.m.a.g.e. consortium (llnl)
    dna sequencing by: incyte genomics, inc.
    clone distribution: msc clone distribution information can be
    found through the i.m.a.g.e. consortium/llnl at:
    http://image.llnl.gov
    plate: llml10313 row: e column: 06
    high quality sequence stop: 613.
    location/qualifiers
    1..948

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Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NRH_MGC library."

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Db	123	AAATTCCTGCTTACCAAAAATATATTAATGTTGGGCTATGGTGCGATACCTGAAT	182
OY	61	cccaactactcagtagtcgtaagcaacaagaatctcttgaaccctcggaggttgaa	120
Db	183	CCGAGCACTACGAGAGGCTGAGCGAGAGATTCCTTGAACCTGGGAGCGGAGTTGCA	242
OY	121	gttagcccgagatcatgcccactgcaaccagctctgtggcgaaagagcaagactgtgtcaa	180
Db	243	GTGAGCGGAGATCCGCCCACTGCACTCCAGGCTTATGAGTACAGAGCTATGACTCCATCCAA	302
OY	181	a--aaataaagaataataaanaattagagccaggtgtgtgtacacacttacttca	238
Db	303	AAACAACMAAAMAAAAGGCAAGCAGCACTGCCAGGCAACATGATGCACTCCTGTAATCCA	362
OY	239	acaacttggagagctgaggttggagagatcgctgtgaagtcagcatttaagaatcgctag	298
Db	363	GCACTTTGGGAGGCCAAGGCGGGCGAGATCACCTTAAGGTCCGGAGTTTCGAGACCAGCTTGG	422
OY	299	gcaacatagtgaaccttgaactctcaaaaaaattcaaaagttaaatgaaacatgtgtgtgca	358
Db	423	CCAAACATGATGAACCCCGTCTTAC-#AAAATAATACAAAATTAACCTGGGCAATGGTGGCG	481
OY	359	tgtgctgtgaatcttagtctgtcgtcggagagctgaggttggagagatcaatc-acgacaaaga	417
Db	482	CATGCGCTGATGTCGACGACTACTTGGAGAGCTGAGGAGGAGAAATTCCTTGAACCAACGA	541
OY	418	tttcaagagctgcagtgagctgtgatattgatactacgcgaactccagcctcgggtgaca	470
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DEFINITION	HS:A0743787.	942 bp DNA linear GSS 16-JUN-1999
ACCESSION	AS550L.AL.E07.T7A RPII-II Human Male BAC Library Homo sapiens genomic clone Plate=1077 Col=13 Row=1, DNA sequence.	
VERSION	A0743787	
KEYWORDS	A0743787.1 GI:5521309	
SOURCE	GSS.	
ORGANISM	human. Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 942)	
AUTHORS	Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and Hood,L.	
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome	
JOURNAL	Proc. Natl. Acad. Sci. U. S. A.	96 (17), 9733-9744 (1999)
MEDLINE	99380589	
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L	

University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RBC1-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPEC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (<http://info@resgen.com>). BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 1077 row: I column: 13
Seq primer: 17
Class: BAC ends

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			/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRII Methyase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"		
BASE COUNT	283 a	234 c	252 g	168 t	5 others
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OY	1 aaaccgcgacctctacgaataaac-aaaatagcctgtgtgtgtgcttgcactctaa	59			
Dd	336 AAACCCCATCTCTACTATAAAATACAAAAAATTAGGTGGTGGTGCGCATCACCATTAG	395			
OY	60 tcccacccttcaggtagcgacaagaatctcttgaaacctggggggtggaagtgc	119			
Dd	396 TCCGAGCTGCTGGGAGGCTGAGCGGGAGAATGCCCTTCGCACTGGGAGGAGAGGTTGC	455			
OY	120 agtaagccgagatcatlgtccaactcaaccagctctgtggcgacaagagaactctgtctca	179			
Dd	456 AGTGAACCGAGATCGCATCTACTGCACTCCAGGCTGGGCGAGACAAGACACTCCATCTTA	515			
OY	180 aaaataaagataataaaaaaatlagagggcagtgctgtgtcaacctgtactctcaa	239			
Dd	516 AAAAAAAAAAAAAAAAA-----GGGTGTGTGTGCTCACACTGTAAITCCAG	566			
OY	240 caacttggagagctbaggtlgygagatcgcttgaagtcaggatctaagacatcctlagg	299			
Dd	567 CACTTTGGGAGGCCCAAGGAGGGCAGACATCCCTGAGGTGGGAGTTCAAGACACAGCTGCAC	626			
OY	300 caacatagtgaaccttgaactctacaaaaaaaaattcaaaagttaatggagacatggtgcat	359			
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Dd	685 ATGCGGGTATATCCACAGCTACTCGGGAGGCGGAGCGAGAGATCACTTAACCCGGGAGA	744			
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Dd	745 CAGAGGTTCACTGAGCCAGCATCAAGCCATTGCACTCCAGCTGGGTGACAGAGTAGAGA	804			
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LOCUS	AUI55227/c				
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ACCESSION	AUI55227				
VERSION	AUI55227.1				
KEYWORDS	GI:11016748				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
	1 (bases 1 to 500)				
	Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Sugano				
	Yamamoto,T., Wakamatsu,A., Ozawa,M., Nakamura,Y., Nagai,T., Sugano				

TITLE	S. and Isogai,T.). HII human cDNA project (Oka,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura,T., Nagai,T., Sugano,S., Isogai,T.)					
JOURNAL	Unpublished (2000)					
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3951 Fax: 81-438-52-3952 Email: genomcs@hri.co.jp HRI Human cDNA Project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.					
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OY	304 atagtgaagaccttgactctcacaanaaatltaaaagttaatgagacatggtgatgtgc 363					
DB	184 ATGGTGAATTCCTGCTCTACTAAANA--TACAATAATTGACGAGCGGTGTGTGCACGC 127					
OY	364 cgtgtacttaagtctgtgtgggaggtcgtgaagttgggaagatcaacttaagacagagattcaa 423					
DB	126 CGTGAATCCACCCCACTTTGGAGGCTGAGAGGTGGGAATAATCGCTTGAACCCAGAGGCAGA 67					
OY	424 ggctgcagtgagctgtgattgatacactgcaactccagccttggtgaagaagtggagccttg 483					
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DEFINITION	MR2-HN0035-141200-015-c05 HN0035 Homo sapiens cDNA, mRNA sequence.					

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 REFERENCE 1 (bases 1 to 568)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brlones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J..
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-HN0035-141200-015-c05&t3=2000-12-14&t4=1)
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 BASE COUNT 168 a 126 c 161 g 113 t
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 DB 65 CTACTCGGGGGCTGAGGAGGAGGATCGCTTGAGTCAGGAGGAGGAGGAGGAGGAG 124
 QY 126 ccgagatcatgcaacgcaaccagctctgggacagagcaagactcttcaaaaat 185
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 DB 125 CCAAGATCGTGCACCTGCAGGCTGGGCGACAGACGAGACTCGCTCAAAATTA 184
 QY 186 aagaataaataaataatlagagccagggtgtgtcacaacctgtactcaacatt 245
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 DB 185 ATAAATTAATAAATAAATCTCTGGCCAGGCGGCTCATGGCTGTAAATCCAGCACTTT 244
 QY 246 gggaggtcagagtggaagatcgcttgaagtgagcatttaagacatgctaggaacat 305
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 DB 305 GGTGAACCCCTGTCTCTAC-TAATAATACAAAATTAGCTGGGCGTGAATGTCATGCT 363
 QY 366 gtactcagctctggtggaagctgaggtggaagatcaacttacgaccagattcaag 425
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 DB 364 ATAGTCCACACTACTTGGGGGCTGAGGACGAGATCGCTGAATTCGGAGGTGAGG 423
 QY 426 ctacagtagctgtgttgcacacacacacacacacacacacacacacacacacac 484
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 DB 424 TTGCATGAGCCCAAAATTATGCCACTGCACTCCAGCTGTGCAACGAGTGAAGTCTGT 483
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Search completed: October 8, 2002, 01:41:15
 Job time: 5366 sec

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3	254	50.7	14747	US-09-608-2855-42	Sequence 42, Appl1
4	254	50.7	15977	US-09-608-2854-59	Sequence 59, Appl1
5	251	50.1	6769	US-08-407-784-20	Sequence 20, Appl1
6	251	50.1	6769	US-08-483-553-20	Sequence 20, Appl1
7	251	50.1	6769	US-08-487-002-20	Sequence 20, Appl1
8	251	50.1	6769	US-08-483-5548-20	Sequence 20, Appl1
9	251	50.1	6769	US-08-488-011B-20	Sequence 20, Appl1
10	251	50.1	6769	US-08-850-727-20	Sequence 20, Appl1
11	251	50.1	6769	PCT-US95-10202-20	Sequence 20, Appl1
12	251	50.1	6769	PCT-US95-10203-20	Sequence 20, Appl1
13	251	50.1	6769	PCT-US95-10220-20	Sequence 20, Appl1
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15	247.6	49.4	7620	US-07-767-135-1	Sequence 1, Appl1
16	247.6	49.4	7620	US-07-841-652-1	Sequence 1, Appl1
17	246.2	49.1	14796	US-08-975-080-35	Sequence 35, Appl1
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23	241.2	48.1	4803	US-09-197-636-3	Sequence 3, Appl1
24	241	48.1	4853	US-08-881-450A-22	Sequence 22, Appl1
25	238.6	47.6	8409	US-09-167-681-37	Sequence 37, Appl1
26	235.8	47.1	19736	US-09-740-035-3	Sequence 3, Appl1
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C 31	231.6	46.2	299.7	4	US-09-332-878-5	Sequence 5, Applt
C 32	226.2	45.1	2248.1	4	US-08-367-841A-43	Sequence 43, Applt
C 33	226.2	45.1	2248.1	5	PCR-US95-07201-43	Sequence 43, Applt
C 34	225.6	44.9	5549.3	2	US-08-687-080-101	Sequence 101, Applt
C 35	225.6	44.9	1161.3	4	US-08-484-044-10	Sequence 10, Applt
C 36	222.8	44.5	5352.6	3	US-08-658-136-2	Sequence 2, Applt
C 37	222.8	44.5	5357.7	3	US-08-658-136-1	Sequence 1, Applt
C 38	222.6	44.4	1529.7	4	US-09-817-180-3	Sequence 3, Applt
C 39	220.6	44.0	4035.5	3	US-09-053-866-1	Sequence 1, Applt
C 40	220.6	44.0	3895.5	3	US-08-726-725-2	Sequence 2, Applt
C 41	217.4	43.4	1278.8	3	US-08-509-965C-4	Sequence 4, Applt
C 42	216.8	43.3	7299.8	2	US-09-009-913-1	Sequence 1, Applt
C 43	216.6	43.2	3157.1	3	US-08-323-443B-1	Sequence 1, Applt
C 44	216.6	43.2	7260.4	4	US-09-268-992-7	Sequence 7, Applt
C 45	216.4	43.2	4576.1	1	US-08-632-083-49	Sequence 49, Applt

ALIGNMENTS

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1 RESULT
2 US-09-173-914-6/c
3 : Sequence 6, Application US/09173914
4 : Patent No. 6171857
5 : GENERAL INFORMATION:
6 : APPLICANT: Hendrickson, Eric
7 : TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and
8 : FILE REFERENCE: B0877/7017/MK
9 : CURRENT APPLICATION NUMBER: US/09/173,914
10 : CURRENT FILING DATE: 1998-10-16
11 : EARLIER APPLICATION NUMBER: 60/064,557
12 : EARLIER FILING DATE: 1997-10-17
13 : NUMBER OF SEQ ID NOS: 35
14 : SOFTWARE: FastSeq for Windows Version 3.0
15 : SEQ ID NO 6
16 : LENGTH: 14636
17 : TYPE: DNA
18 : ORGANISM: Homo Sapiens
19 : US-09-173-914-6

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Query Match	54.3%;	Score 272.2;	DB 4;	Length 14636;
Best Local Similarity	74.5%;	Pred. No. 1.5e-73;		
Matches 369;	Conservative 0;	Mismatches 123;	Indels 3;	Gaps 2

Qy	1	aaaccgcgactcagcaaatatcaaaaaatlagcttggttggtgtgcctctaatt	60
Db	12738	AAAOCCCGTCTCTACATAAATAATCAAAAAATTAGCCAGGCATGGTGGCAGATGGCTGTAAAT	12679
Qy	61	ccacactactcagtagtgcgtaagcacaagaatctcttgaaaccttggaagtggaagtttgc	120
Db	12678	CCCAAGCTACTCAAGAGAGGCTGAGAGGAGGAAATCGCTTAACTCTGGAGACAGAAAGTTGGA	12619
Qy	121	gtaagccgaatcatatgccactgcaaacccagctctggtgcagacagacagactcgtctcaa	180
Db	12618	GTGAGCCGAGATTTGGCCACTGCTGACTCCAGCCTGAAATGACAGAAACAAGACTGTGTCAA	12559
Qy	181	aaataaagaatataataaaaaaatttagagggccaggttggtgtctacacctgtactctcaac	240
Db	12558	AAAAAGAAACAAAAGAAAAAATATGGGCGCGGGCGGGGCTCTACACTGTAAATCCAGC	12495
Qy	241	actttgagaggtcgtgaggttgtagagatcgcgttlnaagtcagattaaagacatgctctagac	300
Db	12498	ACTTTGGAGAGCGGAGCGGGCGGAGATCAAC--CAGSTCAGAGAGATCGAGACATCCGGCT	12441
Qy	301	aactagtgtgagacttgcactctacaaaaaaattcaaaaagttaagtgaacatgltgtgcag	360
Db	12440	AAAACGGTGAACCTCGTCTCTACTAAATATCAAAAAATTATGCCGGGCGTAAGTGGGG	12381

Qy	361	tgccctgaagtcctcagctgctcgggagagagcgtgaagcttgagagagctacttaagcagcaagattt	420
Db	12380	CGCCTGAGTCCAGCTACTTGGAGGCGTGAACGACGAGAGATGGCGTGAACCCGGGAGGC	12321
Qy	421	caagagcgcagcagctagctgtgattgtatgcatcaactgcgaatccagcct-gtgtgacagagctagaagc	479
Db	12320	GGAGCTTGCAGTAGCGCCGAGATCCGCCACTGCACCTCCAGGCTTGGGCAGACGAGCAGAC	12261
Qy	480	cctgctcacaacaaa	494
Db	12260	TCCTCTCAAAAAA	12246

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RESULT      2
US-09-608-285A-8/C
; Sequence 8, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 08/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 9365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (3405)
; OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
; NAME/KEY: misc.feature
; LOCATION: (9214)
; OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
; NAME/KEY: misc.feature
; LOCATION: (9303)
; OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
; NAME/KEY: misc.feature
; LOCATION: (9311)
; OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
; US-09-608-285A-8

Query Match          50.7%; Score 254; DB 4; Length 9365;
Best Local Similarity 69.8%; Pred. No 4,6e-68;
Matches 345; Conservative 30; Mismatches 101; Indels 18; Gaps 3;

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Db	7929	TACAAAAAATATAGACAAGAGTGTGGCACACCGTATATCCAGGACTACAGAGGCT	7870
QY	80	aagcacaagaatctcttgaacctgggaagtgagggttcgagtaagccgagatcatgcga	139
Db	7869	GNGTGGGAGGGGTACTTGTGAACCGGGGAGGACAGAGGTTCGATGAACTGAATATATCCA	7810
QY	140	ctgcgaaccagctctggcgacagaagaagactctcctcaaaaaataaagaatlaatatua	199
Db	7809	CTGCACATCCAGCAGATGGGTGACAGACGACAAACCGCTCTCAAAAAAADGAA	7750
QY	200	-----aaattagaagccgggtgttggtccaaacctgtacatcttaaacctt	24
Db	7749	AAAAAAGMAGMAGMAAAAAAGCTGAGGAGTGGTGGCTCATRCCTRTAATTCAGCACTT	7690
QY	245	tgggaagcctgaagtgvggaagatcgccttgaagtcaggaatlaagacatgcctagaacaa	304
Db	7689	TGGGAGCGYGGGCGGTGTGATCCTTGAGTCAARACTGTATACAAATGACAGCGTGGCAACA	7630
QY	305	tagtgaagaccttacctac--aaaaaatctcaagaagttaatgaagacttgctgcacgtgc	363
Db	7629	TGTGGAACACCCCGCTCTTACTATAAAATACAAAAAATTAGCCRGGCTGGTGGCGCHYG	7570
QY	364	cttgaagcttaagctctgggaagcctgaagtggaagatactaatcaagcaagattcca	423
Db	7569	CTGTAAATCCAGCTACTYGGGAGCGTGAAGGCGRAGATCCCTTGAACCAAGAGAGGYRA	7510
QY	424	ggctcgagctagctgtgatcttgaatcaactgaatcaagctgtga--cagaagggccc	481
Db	7509	GGTTCAGTAGTGCAGCATCRCCATYGCACCTCCAGCTTGGMAACAAGACGACATC	7450
QY	482	tgcttcaaaaaaat	495
Db	7449	CGTCTCAAAAAAAT	7436

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RESULT 3
US-09-608-285A-42/c
; Sequence 42, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/353,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/451,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42
LENGTH: 14747

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? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc.feature
? LOCATION: (13671)
? OTHER INFORMATION: n = adenosine or guanine or cytosine or thymidine
?S-09-608-285A-42

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Query Match	50.7%;	Score 254;	DB 4;	Length 14747;
Best Local Similarity	69.8%;	Pred. No. 5.6e-68;		
Matches 345;	Conservative	30;	Mismatches 101;	Indels 18; Gaps 3

[illegible]

RESULT 4
US-09-608-285A-59/C
Sequence 59, Application US/09608285A
Patent No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: 09/US99/16180
PRIOR FILING DATE: 1999-07-16

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Query Match	50.7%	Score 254	DB 4	Length 15977
Best Local Similarity	69.8%	Pred. No. 5.7e-66		
Matches 343	Conservative	30	Mismatches 101	Indels 18
			Gaps	3
QY 20	tatcaaaaattagccctgggtgctggtcttgacacctcaaccataccactactagtagct	79		
Db 12519	TACAAAAAATTTAGACAAAGATGGTGGACACACCTGTAAATCCAGCTACTCAGAGGCT	12460		
QY 80	aaggacaaaataactctttaaccttgaggaggtggaggttggcgttaagccgagatcatgcca	139		
Db 12459	GAGGTGGGAGGCTACCTTGACACCCGGGAGGACAGAGGTGGCAGTAACTGAGATCATGCCA	12400		
QY 140	ctgnaaacccagcttggcgcgacagagcaagaactctgtctcacaanaataaagaatnaa	199		
Db 12399	CTGCACCTCCAGCATGGGTGATACAGACAAACCCCTGTCTCAAAAAAAAAAAAAAAAA	12340		
QY 200	-----aaattagagccaaggtgtggtccaactgactgaactctcaaacct	244		
Db 12339	AAAAAAGAACMGACMAAAAAAGCGCTGGGGTGGTGGCTTCATCCTTAAATTCYTAGACCTT	12280		
QY 245	tgggagagcttaagg tgggagagatgcgtcttgaaagtcagagcatttaagaacatgcgttaga	304		

Oy	12279	TGGAGGCGYACGAGYGCGTGAATCTACTACAGRGCAGRAAGTTTAAAGTAAGCTGGCCACA	12220
Oy	305	tagtgaaccttgaactctac-aaaaaatcaaaagtaatgagaacatggtagcatgtgc	363
Db	12219	TGGGAAAACCCCCTCTCTCTCTATAAATCAAAAAATTAGCCRCGCCGTGGTCGRYAC	12160
Oy	364	cttgtaagtcctaagcttgtcgtggaggagcgctggaqgttggaggatacttaacgaccgatattcaa	423
Db	12159	CTGTAATACCAGCTACTTGGAGGCGCTGAGGCGCAGRGAGAATGCGTTTGAAACCCAGGAGGYGRA	12100
Oy	424	ggctgcagbtgaactgtgtgatgtcatactgaactgcacccagctgtgtba--cagaatgagagccc	481
Db	12099	GGYGCGAGTAGYGMWATCRYGCCATYGCACCTCCAGCCYKGGMAACAGAGCRAAGCTC	12040
Oy	482	tgctcacaaaatat 495	
Db	12039	CGTCTCAAAAAAT 12026	
 RESULT 5 US-08-480-784-20 ; Sequence 20, Application US/08480784 ; Patent No. 5693473 GENERAL INFORMATION: APPLICANT: Skolnick, Mark H. APPLICANT: Goldgar, David E. APPLICANT: Miki, Yoshio APPLICANT: Swenson, Jeff APPLICANT: Kamb, Alexander APPLICANT: Harshman, Keith D. APPLICANT: Shatluck-Eldens, Donna M. APPLICANT: Tavligian, Sean V. APPLICANT: Wiseman, Roger W. APPLICANT: Futreal, P. Andrew TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer TITLE OF INVENTION: Susceptibility Gene NUMBER OF SEQUENCES: 85 CORRESPONDENCE ADDRESS: ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000 CITY: Washington STATE: DC COUNTRY: USA ZIP: 20005 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/480,784 FILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/409,305 FILING DATE: 24-MAR-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/348,824 FILING DATE: 29-NOV-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/308,104 FILING DATE: 16-SEP-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/300,266 FILING DATE: 02-SEP-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/289,221 FILING DATE: 12-AUG-1994 ATTORNEY/AGENT INFORMATION: NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957 REFERENCE/DOCKET NUMBER: 24884-109347			

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6769 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPERETHERICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-480-784-20

Query Match          50.1%; Score 251; DB 1; Length 6769;
Best Local Similarity 74.6%; Pred No. 3,3e-67;
Matches 366; Conservative 0; Mismatches 120; Indels 5; Gaps 4

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OY      302  acatagtgagagccttgactctacataaaaattcaaaagttaaattagagacatgtgtgacatgt 361
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OY      362  gctctgtatcctatgcctgtcgtcgggaggctcgtgagtgagagatcaacttaagcacaggatcttc 421
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OY      422  aaagcttcagatgtagcttgtatgtcatcaactgtacacgtccagcct-gtgcagagatgtgagcc 480
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; Patent No. 570999
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: MikI, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshman, Keith D.
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Tavligian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
```


[illegible]

RESULT

US-081488-011B-20
: Sequence 20, Application US/08488011B
: Patent No. 5753441
: GENERAL INFORMATION:
: APPLICANT: Skolnick, Mark H.
: APPLICANT: Goldgar, David E.
: APPLICANT: Miki, Yoshio
: APPLICANT: Swenson, Jeff
: APPLICANT: Ramb, Alexander
: APPLICANT: Harshman, Keith D.
: APPLICANT: Shattuck-Eldens, Donna M.
: APPLICANT: Tavtiglian, Sean V.
: APPLICANT: Wiseman, Roger W.
: APPLICANT: Futreal, P. Andrew
: TITLE OF INVENTION: 1q-Linked Breast and Ovarian Cancer
: TITLE OF INVENTION: Susceptibility Gene
: NUMBER OF SEQUENCES: 85
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
: STREET: 1201 New York Avenue, N.W., Suite 1000
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/488,011B
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/409,305
: FILING DATE: 24-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/348,824
: FILING DATE: 29-NOV-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/308,104
: FILING DATE: 16-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/300,266
: FILING DATE: 02-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/289,221
: FILING DATE: 12-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Imnen, Jeffrey L.
: REGISTRATION NUMBER: 28,957

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1 REFERENCE/DOCKET NUMBER: 24884-109347-09
2
3 TELECOMMUNICATION INFORMATION:
4
5 TELEPHONE: 202-962-4810
6
7 TELEFAX: 202-962-8300
8
9 INFORMATION FOR SEQ ID NO: 20:
10
11 SEQUENCE CHARACTERISTICS:
12
13 LENGTH: 6769 base pairs
14
15 TYPE: nucleic acid
16
17 STRANDEDNESS: double
18
19 TOPOLOGY: linear
20
21 MOLECULE TYPE: DNA (genomic)
22
23 HYPOTHETICAL: NO
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25 ANTI-SENSE: NO
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27 ORIGINAL SOURCE:
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29 ORGANISM: Homo sapiens
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31 OS-08-488-011B-20

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Query Match	50.18;	Score 251;	DB 1;	Length 6765;
Best Local Similarity	74.68;	Pred. No. 3.3e-67;		
Matches 368; Conservative	0;	Mismatches 120;	Indels 5;	Gaps 4

[illegible]

RESULT 10

US-08-850-727-20
 : - Sequence 20, Application US/08850727
 : Patent No. 6182897
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Skolnick, Mark H.
 : APPLICANT: Goldfar, David E.
 : APPLICANT: Miki, Yoshio
 : APPLICANT: Swenson, Jeff
 : APPLICANT: Kemp, Alexander
 : APPLICANT: Harshman, Keith D.
 : APPLICANT: Shattuck-Eidens, Donna M
 : APPLICANT: Tavtigian, Sean V.
 : APPLICANT: Wiseman, Roger W.

```

1  APPLICANT: Futreal, P. Andrew
2  TITLE OF INVENTION: 17g-linked Breast and Ovarian Cancer
3  TITLE OR INVENTION: Susceptibility Gene
4  NUMBER OF SEQUENCES: 85
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
7  STREET: 1201 New York Avenue, N.W., Suite 1000
8  City: Washington
9  STATE: DC
10 COUNTRY: USA
11 ZIP: 20005
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: PatentIn Release #1.0, Version #1.30
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/850,727
20 FILING DATE:
21
22 CLASSIFICATION:
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 08/483,554
25 FILING DATE: 07-JUN-1995
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 08/348,824
28 FILING DATE: 29-NOV-1994
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: US 08/308,104
31 FILING DATE: 16-SEP-1994
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER: US 08/300,266
34 FILING DATE: 02-SEP-1994
35 PRIOR APPLICATION DATA:
36 APPLICATION NUMBER: US 08/289,221
37 FILING DATE: 12-AUG-1994
38 ATTORNEY/AGENT INFORMATION:
39 NAME: Ihnen, Jeffrey L.
40 REGISTRATION NUMBER: 28,957
41 REFERENCE/DOCKET NUMBER: 24884-109347
42 TELECOMMUNICATION INFORMATION:
43 TELEPHONE: 202-962-4810
44 TELEFAX: 202-962-8300
45 INFORMATION FOR SEQ. ID NO.: 20:
46 SEQUENCE CHARACTERISTICS:
47 LENGTH: 6769 base pairs
48 TYPE: nucleic acid
49 STRANDEDNESS: double
50 TOPOLOGY: linear
51 MOLECULE TYPE: DNA (genomic)
52 HYPOTHETICAL: NO
53 ANTI-SENSE: NO
54 ORIGINAL SOURCE:
55 ORGANISM: Homo sapiens
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57 US-08-850-727-20

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3      : Sequence 20, Application PC/TUS9510202
4      :
5      : GENERAL INFORMATION:
6      : APPLICANT: Shatluck-Eldens, Donna M.
7      : APPLICANT: Simard, Jacques
8      : APPLICANT: Emi, Mitsuru
9      : APPLICANT: Nakamura, Yasuue
10     : APPLICANT: Durocher, Francine
11     : TITLE OF INVENTION: In Vivo Mutations and Polymorphisms
12     : TITLE OF INVENTION: in the 17q-linked Breast and Ovarian Cancer
13     : TITLE OF INVENTION: Susceptibility Gene
14     : NUMBER OF SEQUENCES: 85
15     :
16     : CORRESPONDENCE ADDRESSES:
17     : ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
18     : STREET: 1201 New York Avenue, N.W., Suite 1000
19     : CITY: Washington
20     : STATE: DC
21     : COUNTRY: USA
22     : ZIP: 20005
23     :
24     : COMPUTER READABLE FORM:
25     : MEDIUM TYPE: Floppy disk
26     : COMPUTER: IBM PC compatible
27     : OPERATING SYSTEM: PC-DOS/MS-DOS
28     : SOFTWARE: patentin Release #1.0, Version #1.30
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31     : FILING DATE:
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33     : PRIOR APPLICATION DATA:
34     : APPLICATION NUMBER: US
35     : FILING DATE: 07-JUN-1995
36     : PRIOR APPLICATION DATA:
37     : APPLICATION NUMBER: US 08/409,305
38     : FILING DATE: 24-MAR-1995
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41     : FILING DATE: 29-NOV-1994
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47     : FILING DATE: 02-SEP-1994
48     : PRIOR APPLICATION DATA:
49     : APPLICATION NUMBER: US 08/289,221
50     : FILING DATE: 12-AUG-1994
51     : ATTORNEY/AGENT INFORMATION:
52     : NAME: Ihnen, Jeffrey L.

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PCT-US95-10220-20
; Sequence 20, Application PC/TUS9510220
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: MIKI, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshman, Keith D.
; APPLICANT: Shattuck-Bidens, Donna M.
; APPLICANT: Tavligian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
; TITLE OF INVENTION: Method for diagnosing a
; TITLE OF INVENTION: Predisposition for Breast and Ovarian Cancer
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10220
; FILING DATE:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/409,305
; FILING DATE: 24-MAR-1995
; APPLICATION NUMBER: US 08/348,824
; FILING DATE: 29-NOV-1994
; APPLICATION NUMBER: US 08-308,104
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/300,266
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,221
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109347
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6769 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
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Query Match 50.1% Score 251; DB 5; Length 6769;
Best Local Similarity 74.6%; Pred. NO. 3.3e-67;
Matches 368; Conservative 0; Mismatches 120; Indels 5; Gaps 4;
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; Sequence 28, Application US/09564805
; Patent NO. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavligian, Sean V.
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Best Local Similarity	72.1%;	Pred. No. 3.8e-66;		
Matches 369;	Conservative	0;	Mismatches 129;	Indels 14;
				Gaps 3;

[illegible]

Search completed: October 8, 2002, 03:43:03
Job time: 12278 sec

US-07-767-135-1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Run on:      October 8, 2002, 03:42:14 ; Search time 648.94 Seconds
            (Without alignments)
            1063.580 Million cell updates/sec
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Perfect score: 402
Sequence: 1 gatctgcactgagctcct.....cattcagatgtattatgag 402
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scoring table: IDENT111_NOC
Gapop 10.0 , Gapext 1.0

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Searched: 1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 3472872
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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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23:	/SIDS1/gcgdata/genseq/genseqn-emb1/NA2001B.DAT.*
24:	/SIDS1/gcgdata/genseq/genseqn-emb1/NA2002.DAT.*

SUMMARIES

Result	Query	Match	Score	No	Description
	AA293705	21	18402	402	CYB5P fatty acid
	AAV34206	19	1478	343	Human secreted pro
	AAV99727	22	1772	343	Human protein enco
	AAV34462	19	85.3	342.6	Human secreted pro
	CYB5P fatty acid	21	1700	341.4	CYB5P fatty acid
	Human fatty acid d	21	1757	330	Human fatty acid d
	DNA encoding novel	23	1663	290	DNA encoding novel
	Human gene signatu	16	208	186	Human gene signatu
	DNA encoding novel	23	502	146	DNA encoding novel

C	10	142.4	35.4	347	22	AAFB68420	Human Lung tumour
11	55.2	13.7	29521	22	AAS32517	Human genomic DNA	
12	55.2	13.7	29543	22	AAS32516	Human genomic DNA	
13	45.4	11.3	560	22	AAH05345	Human cDNA clone (
14	45.4	11.3	1474	21	AAAF1845	Human breast and o	
15	45.4	11.3	1686	19	AAAG63641	Confit 2511785 enc	
16	45.4	11.3	1686	20	AAAG60908	Human desaturase g	
17	45.4	11.3	1686	20	AAAB82640	Confit 2511785 enc	
18	45.4	11.3	1686	21	AAA49937	Human delta-5-desat	
19	45.4	11.3	1686	21	AAA09451	Human confit DNA e	
20	45.4	11.3	1686	21	AAAL4592	Nucleotide sequenc	
21	45.4	11.3	1843	19	AAAB63642	Confit 2535 encodi	
22	45.4	11.3	1843	20	AAAO0909	Human desaturase g	
23	45.4	11.3	1843	20	AAAB2641	Confit 2535 encodi	
24	45.4	11.3	1843	21	AAA44938	Human delta-5-desat	
25	45.4	11.3	1843	21	AAA09452	Human confit DNA e	
26	45.4	11.3	1843	21	AAAL4593	Nucleotide sequenc	
27	45.4	11.3	2166	22	AAAH15815	Human cDNA sequenc	
28	45.4	11.3	2166	22	AAAH15815	Human cDNA sequenc	
29	45.4	11.3	2257	19	AAAB63643	Confit 253538a enc	
30	45.4	11.3	2257	20	AAAO0910	Human desaturase g	
31	45.4	11.3	2257	20	AAAB2642	Confit 253538a enc	
32	45.4	11.3	2257	21	AAA44939	Human delta-5-desat	
33	45.4	11.3	2257	21	AAA09453	Human confit 2535	
34	45.4	11.3	2257	21	AAAL4594	Nucleotide sequenc	
35	45.4	11.3	2258	22	AAAG94786	Human full-length	
36	45.4	11.3	2825	22	AAAG94377	Human full-length	
37	45.4	11.3	3083	22	AAAG94346	Human full-length	
38	45.4	11.3	3106	21	AAAG6019	Human ORFX ORF1574	
39	45.4	11.3	3184	21	AAAZ4247	Human oxidoreducta	
40	45.4	11.3	4089	21	AAAG90543	Human fatty acid d	
41	45	11.2	596	22	AAH05664	Human cDNA clone (
42	43.8	10.9	2190	22	AAH16118	Human cDNA sequenc	
43	40.6	10.1	1335	22	AAAD19403	Human delta-6-desat	
44	38	9.5	1335	22	AAIB6599	Rat fatty acid desat	
45	38	9.5	1335	22	AAID19402	Rat delta-6-desatur	

ALIGNMENTS

RESULT	1
AA293705	
ID	AA293705 standard; DNA; 18402 BP.
XX	
AC	AA293705;
DJ	16-AUG-2000 (first entry)
XX	
DE	CYB5RP fatty acid desaturase gene.
XX	
KW	CYB5RP: fatty acid desaturase; cytochrome b5; macular degeneration;
KW	skin disease; diabetes; inflammation; autoimmune disease;
KM	cardiovascular disease; viral infection; virus; identification;
human; ss.	
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	TATA_box
FT	
FT	exon
FT	
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FT	/label= Exon 1
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FT	11884..12414
FT	/tag= e
FT	/label= intron 2
FT	

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FT      exon      12415..12612
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FT      12613..13076
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FT      /label= Intron 3
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FT      polyA_signal
FT      WO200021557-A1.
FT      20-APR-2000.
FT      05-OCT-1999; 99WO-US23253.
FT      09-OCT-1998; 98US-0103760.
FT      (MERI ) MERCK & CO INC.
FT      Petrukhin K, Caskey CT;
FT      WPI; 2000-317847/27.

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XX      Novel cytochrome b5-related protein useful for identifying modulators
PT      of useful for treating retinal dysfunction such as macular degeneration,
PT      skin diseases, diabetic complications and cardiovascular disorders
XX      Claim 2; Figure 2; 44pp; English.
XX      CYB5RP is a fatty acid desaturase and a cytochrome b5-related protein.
CC      Pharmaceutical compositions comprising an activator or an inhibitor of
CC      CYB5RP protein are useful for treating macular degeneration. The
CC      CYB5RP protein is useful for identifying its activators or inhibitors
CC      which are useful for treating abnormal conditions associated with
CC      CYB5RP protein activity such as skin disease, diabetic complications,
CC      inflammatory and autoimmune disorders, cardiovascular disorders and
CC      complications of viral infection, large amounts of valuable essential
CC      fatty acids can be produced by the expression of CYB5RP protein.
XX      Sequence 18402 BP; 3790 A; 5122 C; 5428 G; 4062 T; 0 other;
SQ
Query Match      100.0%; Score 402; DB 21; Length 18402;
Best Local Similarity 100.0%; Pred. No. 1.3e-104;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 gatcttgcaactgagctccttaacacccaccactgcccaccaccacccaggtccct 60
DB      18000 gatcttgcaactgagctccttaacacccaccaccactgcccaccaccacccaggtccct 18059
QY      61 gaagaagctctgtgacatctgtctgagcgcctacactcactcagtgaaaggaacaccagg 120
DB      18060 gaagaagctctgtgacatctgtctgagcgcctacactcactcagtgaaaggaacaccagg 18119
QY      121 cgggcagagaaggggtcctcaggcagccagcaacccaagcccccggcgagtcgatatccc 180
DB      18120 cgggcagagaaggggtcctcaggcagccagcaacccaagcccccggcgagtcgatatccc 18179
QY      181 ccacccctccactgagccagcctcgggggtgcctctgctgcctccctcgtgactgtcttc 240
DB      18180 ccacccctccactgagccagcctcgggggtgcctctgctgcctccctcgtgactgtcttc 18239
QY      241 cccttgccccctcaatgtgtatttcacagagccctatggtccttgctctggcctcgtatgg 300
DB      18240 cccttgccccctcaatgtgtatttcacagagccctatggtccttgctctggcctcgtatgg 18299
QY      301 gacaggggtagaagggaaggtgagcatatttcctcagagcgagatgggggaaag 360
DB      18300 gacaggggtagaagggaaggtgagcatatttcctcagagcgagatgggggaaag 18359
QY      361 cgttatatttatataaataacattcagatgtattatggag 402
DB      18360 cgttatatttatataaataacattcagatgtattatggag 18401
RESULT      2
ID      AAV34206 standard; DNA; 1478 BP.
AC      AAV34206;
XX      28-JAN-1999 (first entry)
DE      Human secreted protein gene 53 clone HSKDM02.
XX      Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW      diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW      developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW      immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW      inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW      cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW      osteoporosis; arthritis; testis; lung; thyroiditis; thyroid digestion;
KW      endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX      Homo sapiens.
OS

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PR 22-AUG-1997; 97US-0056862.
 PR 22-AUG-1997; 97US-0056864.
 PR 22-AUG-1997; 97US-0056872.
 PR 22-AUG-1997; 97US-0056874.
 PR 22-AUG-1997; 97US-0056875.
 PR 22-AUG-1997; 97US-0056876.
 PR 22-AUG-1997; 97US-0056877.
 PR 22-AUG-1997; 97US-0056878.
 PR 22-AUG-1997; 97US-0056879.
 PR 22-AUG-1997; 97US-0056880.
 PR 22-AUG-1997; 97US-0056881.
 PR 22-AUG-1997; 97US-0056882.
 PR 22-AUG-1997; 97US-0056884.
 PR 22-AUG-1997; 97US-0056886.
 PR 22-AUG-1997; 97US-0056887.
 PR 22-AUG-1997; 97US-0056888.
 PR 22-AUG-1997; 97US-0056889.
 PR 22-AUG-1997; 97US-0056892.
 PR 22-AUG-1997; 97US-0056893.
 PR 22-AUG-1997; 97US-0056894.
 PR 22-AUG-1997; 97US-0056903.
 PR 22-AUG-1997; 97US-0056908.
 PR 22-AUG-1997; 97US-0056909.
 PR 22-AUG-1997; 97US-0056910.
 PR 22-AUG-1997; 97US-0056919.
 PR 05-SEP-1997; 97US-0056911.
 PR 05-SEP-1997; 97US-0057650.
 PR 05-SEP-1997; 97US-0057651.
 PR 05-SEP-1997; 97US-0057761.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
 PI Feng P, Ferrie AM, Fischer CL, Graves KA, Greene JM, Hu JS;
 PI Kray H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
 PI Ruden SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
 DR WPI: 1998-609887/51.
 DR P-PSDB: AAW75109.
 XX
 PT New isolated human genes and the secreted polypeptides they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 PT
 PT
 PT
 PS Claim 1; Page 208-209; 447pp: English.
 XX
 XX This sequence represents a nucleic acid molecule which encodes a
 CC secreted human protein. The gene number, and the clone it is derived
 CC from, are detailed in the descriptor line. The gene can be used to
 CC generate fusion proteins by linking to the gene to a human immunoglobulin
 CC Fc portion (e.g. AAV3145) for increasing the stability of the fused
 CC protein as compared to the human protein only.
 CC The invention relates to 70 novel genes and their fragments (nucleic
 CC acid sequences: AAV34154-V34276; amino acid sequences AAW75057-AW75179)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 70
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV34154 for described uses).
 CC
 XX
 XX Sequence 1478 BP; 299 A; 470 C; 395 G; 311 T; 3 other:
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 Query Match 85.3%; Score 343; DB 19; Length 1478;
 Best Local Similarity 100.0%; Pred. No. 3,7e-88;
 Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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 Db 1086 caggtccctctgaagaagctctgtgtacatctcgtctgaagcgcctaccctcctgaagaagca 1145
 |||
 112 acacccgcggcgagcagaagggctcaaggcacccagcaaccacgaagcgaaccccgcgagga 171
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Db 1146 acaccacgagcgaggaagagctcagggcaccagcaacacgagccccgcgcgga 1205
Oy 172 tcgatacccccccctccactgagcagcctgggggctgcctgcctctgtgact 231
Db 1206 tcgatacccccccctccactgagcagcctgggggctgcctgcctctgtgact 1265
Oy 232 gtgtctccctcgcgcgcctccatcgtgtatctcagcagcctatgacctgtctcg 291
Db 1266 gtgtctccctcgcgcgcctccatcgtgtatctcagcagcctatgacctgtctcg 1325
Oy 292 gccctatggagcagggatagaggaggtgagcctacatcttcctagacgagaatt 351
Db 1326 gccctatggagcagggatagaggaggtgagcctacatcttcctagacgagaatt 1385
Oy 332 ggggggaaagctgtattttatataataacatcagatgta 394
Db 1386 ggggggaaagctgtattttatataataacatcagatgta 1428

RESULT 3

AAH9727/c
ID AAH9727 standard; cDNA: 1772 BP.

AC AAH9727;

DT 16-OCT-2001 (first entry)

DE Human protein encoding cDNA sequence SRF ID NO:562.

XX Human; cancer; HIV infection; human immunodeficiency virus;
XX antiinflammatory; antirheumatic; antirheumatic; immunosuppressive;
XX antibacterial; endocrine; cardiac; central nervous system; virocid;
XX anti-HIV; fungicide; antitumor; cardiovascular; antineoplastic; anaemia;
XX antiaggregant; haemostatic; vulnery; antifungal; osteoporosis; eczema;
XX dermatological; antiallergic; antistimulant; antidiabetic; cytostatic;
XX neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
XX immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
XX anaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
XX cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
XX genetic disease; haematopoietic disorder; platelet disorder; asthma;
XX thrombocytopenia; osteoporosis; severe combined immunodeficiency;
XX allergic rhinitis; diabetes; multiple sclerosis; depression;
XX Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
XX neurological disorder; ss.

OS Homo sapiens.

PN WO200153455-A2.

PD 26-JUL-2001.

PF 22-DEC-2000; 2000WO-US5017.

PR 23-DEC-1999; 99US-0471275.

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PA (HYSE-) HXSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-457603/49.

DR P-PSDB; AAM25786.

PT Isolated human polynucleotides encoding polypeptides, useful for the

XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -

XX Claim 1; Page 608-609; 1217pp; English.

XX AAH9166 to AAH9904 encode the human proteins given in AAM25225 to

CC AAH25963. The proteins can have activities based on the tissues and

CC cells they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiallergic; immunosuppressive; antibacterial; endocrine; cardiac;

CC central nervous system; virocid; anti-HIV; fungicide; antitumor;
CC cardiovascular; antineoplastic; antirheumatic; haemostatic; vulnery;
CC antidiabetic; osteoporosis; dermatological; antiallergic; antineoplastic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.

SO Sequence 1772 BP; 342 A; 518 C; 582 G; 330 T; 0 other;

Query Match 85.3%; Score 343; DB 22; Length 1772;

Best Local Similarity 100.0%; Pred. No. 4e-88;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 112 acaccacgagcgaggaagagctcagggcaccagcaacacgagccccgcgcgga 171
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Oy 172 tcgatacccccccctccactgagcagcctgggggctgcctgcctctgtgact 231
Db 234 TCGATACCCCGACCCCTCCATCGCCAGCTGGGGTGCCTGCCCTCTGTACT 175
Oy 232 gtgtctccctcgcgcgcctccatcgtgtatctcagcagcctatgacctgtctcg 291
Db 174 GTGTCTCCCTCCTCGCCCTCCATCATGTGTATTCAGCAGCCCTATGCGCTGTGG 115
Oy 292 gccctatggagcagggatagaggaggtgagcctacatcttcctagacgagaatt 351
Db 114 GCCGTATGCGAGCAGGGGTAGAGGAAAGCTAGCATATTTCTTACAGCGAATT 55
Oy 352 ggggggaaagctgtattttatataataacatcagatgta 394
Db 54 GGGGGAAGCTGTATTATTTATTAATAATACATTCAGATGTA 12

RESULT 4

AAV34262
ID AAV34262 standard; DNA: 2016 BP.

AC AAV34262;

DT 28-JAN-1999 (first entry)

DE Human secreted protein gene 53 clone HSKDM02.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
XX immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;
XX cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Homo sapiens.

XX MO9839446-A2.

PN

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PD 11-SEP-1998.
XX 06-MAR-1998; 98WO-US04492.
XX
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040336.
PR 07-MAR-1997; 97US-0040626.
PR 11-APR-1997; 97US-0043311.
PR 11-APR-1997; 97US-0043312.
PR 11-APR-1997; 97US-0043313.
PR 11-APR-1997; 97US-0043314.
PR 11-APR-1997; 97US-0043315.
PR 11-APR-1997; 97US-0043568.
PR 11-APR-1997; 97US-0043569.
PR 11-APR-1997; 97US-0043576.
PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043668.
PR 11-APR-1997; 97US-0043670.
PR 11-APR-1997; 97US-0043671.
PR 11-APR-1997; 97US-0043672.
PR 11-APR-1997; 97US-0043674.
PR 23-MAY-1997; 97US-0047492.
PR 23-MAY-1997; 97US-0047500.
PR 23-MAY-1997; 97US-0047501.
PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
PR 23-MAY-1997; 97US-0047581.
PR 23-MAY-1997; 97US-0047582.
PR 23-MAY-1997; 97US-0047583.
PR 23-MAY-1997; 97US-0047584.
PR 23-MAY-1997; 97US-0047585.
PR 23-MAY-1997; 97US-0047586.
PR 23-MAY-1997; 97US-0047587.
PR 23-MAY-1997; 97US-0047588.
PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047592.
PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
PR 23-MAY-1997; 97US-0047599.
PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 23-MAY-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 22-AUG-1997; 97US-0056300.
PR 22-AUG-1997; 97US-0056301.
PR 22-AUG-1997; 97US-0056302.
PR 22-AUG-1997; 97US-0056306.
PR 22-AUG-1997; 97US-0056337.
PR 22-AUG-1997; 97US-0056637.
PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056845.
PR 22-AUG-1997; 97US-0056862.
PR 22-AUG-1997; 97US-0056864.
PR 22-AUG-1997; 97US-0056872.

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PR 22-AUG-1997; 97US-0056874.
PR 22-AUG-1997; 97US-0056875.
PR 22-AUG-1997; 97US-0056876.
PR 22-AUG-1997; 97US-0056877.
PR 22-AUG-1997; 97US-0056878.
PR 22-AUG-1997; 97US-0056879.
PR 22-AUG-1997; 97US-0056880.
PR 22-AUG-1997; 97US-0056881.
PR 22-AUG-1997; 97US-0056882.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.
PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.
PR 22-AUG-1997; 97US-0056893.
PR 22-AUG-1997; 97US-0056894.
PR 22-AUG-1997; 97US-0056903.
PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057761.

(HUMA-) HUMAN GENOME SCI INC.
XX
XX Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
PI Feng P, Fertie AM, Fischer CL, Graves KA, Greene JM, Hu JS;
PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
PI Ruden SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
DR WPI: 1998-609887/51.
XX P-PSDB: AAW75165.
XX
XX New isolated human genes and the secreted polypeptides they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 1; Page 262-264; 447pp; English.
XX
XX This sequence represents a nucleic acid molecule which encodes a
CC secreted human protein. The gene number, and the clone it is derived
CC from, are detailed in the descriptor line. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV34145) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 70 novel genes and their fragments (nucleic
CC acid sequences: AAV34154-V34276; amino acid sequences AAW75057-W75179)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 70
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV34154 for described uses).
XX
XX Sequence 2016 BP; 401 A; 629 C; 563 G; 412 T; 11 other;
XX
XX
XX Query Match 85.2%; Score 342.6; DB 19; Length 2016;
XX Best Local Similarity 99.7%; Pred. No. 5.4e-88;
XX Matches 342; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 52 caggtccctgaagaagtcgtgacatctgacgtgcgaacccatccatcagtgaaagca 111
XX |||||||
XX 1637 caggtccctgaagaagtcgtgacatctgacgtgcgaacccatccatcagtgaaagca 1696
XX
XX 112 aaacccagcgagcagaagaaggtcagggcaccacacacacgaagcccccgcggcgga 171
XX |||||||
XX 1697 aaacccagcgagcagaagaaggtcagggcaccacacacacgaagcccccgcggcgga 1756
XX
XX 172 tcgataccccccaccatccatcgacgtggtgggtgctgcctgcgtccctctctgtact 231

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|||||:|||||
Db 1757 tcgataccccccacccctccacacgctgagggggtgcccctgctgccctccgtact 1816
QY 232 gtgtcttcctcgcccccacacatgtatccagagccctatgacctgtgctcgtg 291
Db 1817 gtgtcttcctcgcccccacacatgtatccagagccctatgacctgtgctcgtg 1876
QY 292 gccctatggagacagggtagagggaggtgagcatagcacatttcctagagcagaatt 351
Db 1877 gccctatggagacagggtagagggaggtgagcatagcacatttcctagagcagaatt 1936
QY 352 gggggaaagctgtatttttatataataacattcagatgta 394
Db 1937 gggggaaagctgtatttttatataataacattcagatgta 1979

RESULT 5
AA293706
ID AA293706 standard; cDNA; 1700 BP.
XX
XX AA293706;
DT 16-AUG-2000 (first entry)
XX
XX CYB5RP fatty acid desaturase cDNA.
DE
XX CYB5RP; fatty acid desaturase; cytochrome b5; macular degeneration;
KW skin disease; diabetes; inflammation; autoimmune disease;
KW cardiovascular disease; viral infection; virus; identification;
KW human; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 71..1406
XX FT /*tag= a
XX FT /product= CYB5RP fatty acid desaturase
XX
XX WO200021557-A1.
XX
XX PD 20-APR-2000.
XX
XX PF 05-OCT-1999; 99WO-US23253.
XX
XX PR 09-OCT-1998; 98US-0103760.
XX
XX PA (MERI ) MERCK & CO INC.
XX
XX PI Petrukhin K, Caskey CT;
XX
XX DR WPI: 2000-317847/27.
XX
XX DR P-PSDB; AAY83229.
XX
XX PT Novel cytochrome b5-related protein useful for identifying modulators
XX useful for treating retinal dysfunction such as macular degeneration,
XX skin diseases, diabetic complications and cardiovascular disorders
XX
XX Claim 2: Figure 3; 44pp; English.
XX
XX CC CYB5RP is a fatty acid desaturase and a cytochrome b5-related protein.
XX Pharmaceutical compositions comprising an activator or an inhibitor of
XX CYB5RP protein are useful for treating macular degeneration. The
XX CYB5RP protein is useful for identifying its activators or inhibitors
XX which are useful for treating abnormal conditions associated with
XX CYB5RP protein activity such as skin disease, diabetic complications,
XX inflammatory and autoimmune disorders, cardiovascular disorders and
XX complications of viral infection, large amounts of valuable essential
XX fatty acids can be produced by the expression of CYB5RP protein.
XX
XX SQ Sequence 1700 BP; 319 A; 560 C; 480 G; 341 T; 0 other;

```

Query Match 84.9%; Score 341.4; DB 21; Length 1700;

```

Best Local Similarity 99.7%; Pred. No. 1.1e-87;
Matches 342; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 52 cagggtcccttgagaagttgttgacatctgtgtagcctactcatcagtgagagca 111
Db 1354 cagggtcccttgagaagttgttgacatctgtgtagcctactcatcagtgagagca 1413
QY 112 aacccagcgaggcagagaaggctcagggcaccacagcaacccaagcccccggcgga 171
Db 1414 aacccagcgaggcagagaaggctcagggcaccacagcaacccaagcccccggcgga 1473
QY 172 tcgataccccccacccctccacacatgtatccagcagccctatgacctgtgctg 231
Db 1474 tcgataccccccacccctccacacatgtatccagcagccctatgacctgtgctg 1533
QY 232 gtgtcttcctcgcccccacacatgtatccagcagccctatgacctgtgctgctg 291
Db 1534 gtgtcttcctcgcccccacacatgtatccagcagccctatgacctgtgctgctg 1593
QY 292 gccctatggagacagggtagagggaggtgagcatagcacatttcctagagcagaatt 351
Db 1594 gccctatggagacagggtagagggaggtgagcatagcacatttcctagagcagaatt 1653
QY 352 gggggaaagctgtatttttatataataacattcagatgta 394
Db 1654 gggggaaagctgtatttttatataataacattcagatgta 1696

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RESULT 6
AAA90954
ID AAA90954 standard; cDNA; 1757 BP.
XX
XX AAA90954;
AC
XX
XX DT 15-JAN-2001 (first entry)
XX
XX DE Human fatty acid desaturase 3 coding sequence.
XX
XX KW Human; fatty acid desaturase; FADS-1; FADS-2; FADS-3; gene therapy;
XX liver disease; coronary artery disease; cancer; ss.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 134..1471
XX FT /*tag= a
XX FT /product= FADS-3
XX
XX PN EP1035207-A1.
XX
XX PD 13-SEP-2000.
XX
XX PF 09-MAR-1999; 99EP-0104664.
XX
XX PR 09-MAR-1999; 99EP-0104664.
XX
XX PA (MULF-) MOLTIGENE BIOTECH GMBH.
XX
XX PI Weber BHF, Margardt A;
XX
XX DR WPI: 2000-559875/52.
XX
XX DR P-PSDB; AAY97540.
XX
XX PT Novel cDNA molecules encoding three human fatty acid desaturases,
XX FADS1, FADS2 and FADS3, useful in the treatment of liver disease,
XX coronary artery disease and cancer -
XX
XX PS Claim 2: Page 38-39; 72pp; English.
XX
XX CC This sequence encodes the human fatty acid desaturase, FADS-3, of the
XX invention. An antibody directed against the 3 FADS molecule of the
XX invention (FADS-1, FADS-2, and FADS-3) is useful for diagnostic or
XX therapeutic purposes. The FADS coding sequences are useful in gene

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CC therapy. The polypeptide and antibodies are useful in screening for
 CC modulating drugs. The polypeptides are also useful for treating liver
 CC disease, coronary artery disease and cancer.
 CC Note: Two copies of the sequence listing are present within this
 CC patent, which contain identical sequences. AAA90952 and AAA90955 are
 CC both stated as being SEQ ID 1. AAA90956-A90971, and AAA90972-A90987 are
 CC stated as being SEQ ID's 7-22.
 XX
 SQ Sequence 1757 BP; 318 A; 580 C; 517 G; 342 T; 0 other;
 Query Match 82.1%; Score 330; DB 21; Length 1757;
 Best Local Similarity 99.7%; Pred. No. 2.1e-84;
 Matches 341; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 52 caggtccctgaagaagctgtgacatctgtgacgacctacatcagtgaaagca 111
 DB 1417 caggtccctgaagaagctgtgacatctgtgacgacctacatcagtgaaagca 1476
 QY 112 acacccagcgaggaagagctgacagcgacagcaagccagcccgccggcgga 171
 DB 1477 acacccagcgaggaagagctgacagcgacagcaagccagcccgccggcgga 1535
 QY 172 tcgatacccccacccctccacacgctgaggggtgacctgacctgacctgact 231
 DB 1536 tcgatacccccacccctccacacgctgaggggtgacctgacctgacctgact 1595
 QY 232 gtgtgttctccctcgccccctccacatgtgtatcagcagccctatgctgtgctgg 291
 DB 1596 gtgtgttctccctcgccccctccacatgtgtatcagcagccctatgctgtgctgg 1655
 QY 292 gctctgtgagacaggggtagaggaagtgagacatagcattctcctagagcgaagaa 351
 DB 1656 gctctgtgagacaggggtagaggaagtgagacatagcattctcctagagcgaagaa 1715
 QY 352 gggggaaagctgtattttatattatataaatacatcagatgt 393
 DB 1716 gggggaaagctgtattttatattatataaatacatcagatgt 1757
 RESULT 7
 AAST4468
 ID AAST4468 standard; cDNA; 1663 BP.
 XX
 AC AAST4468;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #10272.
 KW Human; Chromosome mapping; gene mapping; gene therapy; forensic;
 KW Food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSF-) HYSFO INC.
 XX
 PI Drmanac RT, Liu C, Tang YF;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG10281.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 1; SEQ ID NO 10272; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (II) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1663 BP; 332 A; 538 C; 458 G; 335 T; 0 other;
 Query Match 72.1%; Score 290; DB 23; Length 1663;
 Best Local Similarity 97.1%; Pred. No. 5.5e-73;
 Matches 338; Conservative 0; Mismatches 5; Indels 5; Gaps 4;
 QY 52 caggtccctgaag-aagtcgtgacatctgtgacgacctacatcagtgaaagc 110
 DB 1298 caggtccctgaagaaagctctgacatctgtgacgacctacatcagtgaaagc 1357
 QY 111 aacacccagcgaggaagagctcagggcacccagcaacaagcc-agccccggcg 169
 DB 1358 aacacccagcgaggaagagctcagggcacccagcaacaagccagccccggcg 1417
 QY 170 gatcga--tacccccacccctccactgagcagctgggggtccctgctgccccctgg 227
 DB 1418 gatcgaatccccccacccctccactgagcagctgggggtccctgctgccccctgg 1477
 QY 228 tactgtgtctccctcgccccctccacatgtgtatcagcagccctatgagccttggct 287
 DB 1478 tactgtgtctccctcgccccctccacatgtgtatcagcagccctatgagccttggct 1537
 QY 288 ctgggctgtgagacaggggtagaggaagtgagacatg-cacatttcttaagcga 346
 DB 1538 ctgggctgtgagacaggggtagaggaagtgagacatgacatttcttaagcga 1597
 QY 347 gaattggggaaagctgtattttatattatataaatacatcagatgt 394
 DB 1598 gaattggggaaagctgtattttatattatataaatacatcagatgt 1645
 RESULT 8
 AAT25715
 ID AAT25715 standard; cDNA to mRNA; 208 BP.
 XX
 AC AAT25715;
 XX
 DT 10-OCT-1996 (first entry)
 XX
 DE Human gene signature HUMGS07921.
 XX
 KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
 KW human; cloning; mapping; non-biased library; diagnosis; detection;
 KW cell typing; abnormal cell function; ss.
 XX

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OS Homo sapiens.
XX
XX WO9514772-A1.
XX
XX 01-JUN-1995.
XX
XX 11-NOV-1994; 94MO-JP01916.
XX
XX 12-NOV-1993; 93JP-0355504.
XX
XX (MATS/) MATSUBARA K.
XX (OKUB/) OKUBO K.
XX
XX Matsubara K, Okubo K;
XX
XX WPI, 1995-206931/27.
XX
XX Identifying gene signatures in 3'-directed human cDNA library - e.g.
XX for diagnosis of abnormal cell function, by preparing cDNA that
XX reflects relative abundance of corresp. mRNA in specific human
XX tissues
XX
XX Claim 1: Page 1912; 2245pp; Japanese.
XX
XX A single-stranded DNA (or its complementary strand or the corresp.
XX double-stranded DNA) which comprises one of the 7837 "GS" sequences
XX given in AAT19001-T26837 and which is able to hybridise to part of
XX human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
XX sequences were obtained from 3'-directed cDNA libraries prepared
XX from various human tissues; synthesis of cDNA was initiated from the
XX 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
XX untranslated sequence is unique to a particular mRNA species, almost
XX all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
XX is constructed so as to reflect accurately the relative abundance of
XX different mRNAs in the particular tissue from which it was derived.
XX The appearance frequency of a given GS in a cDNA library can be
XX determined (esp. using primers and probes derived from the GS
XX sequences) as a means of diagnosing abnormal cell function or for
XX recognising different cell types.
XX
XX Sequence 208 BP; 34 A; 56 C; 55 G; 52 T; 11 other;
XX
XX
XX Query Match 46.3%; Score 186; DB 16; Length 208;
XX Best Local Similarity 94.7%; Pred. No. 1.4e-43;
XX Matches 197; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
XX
XX QY 170 gatcgataccccccctccactgagcagctgggggtgcctgctgcctcctgta 229
XX |||||||
XX DB 1 gatcgataccccccctccactgagcagctgggggtgcctgctgcctcctgta 60
XX
XX QY 230 ctgtgtcttccctcgcgcctccacatgtgtattcagagagccctatgctgctct 289
XX |||||||
XX DB 61 ctgtgtcttccctcgcgcctccacatgtgtattcagagagccctatgctgctct 120
XX
XX QY 290 gggcctgattggacagaggttagaggaagtgtacatagacatttccctagagcgagaa 349
XX |||||||
XX DB 121 gggcctgattgng-nagggttagaggaagtgtacatagacatttccctagagcgagaa 179
XX
XX QY 350 ttgggggaaagctgtattttatata 377
XX |||||||
XX DB 180 ttgggggaaagctgtattttatata 207
XX
XX
XX RESULT 9
XX AAS74464
XX ID AAS74464 standard; cDNA; 502 BP.
XX
XX AC AAS74464;
XX
XX XX 13-FEB-2002 (first entry)
XX
XX DE DNA encoding novel human diagnostic protein #10268.

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```

XX
XX KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX P-PsDB; ABG10277.
XX
XX
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 1: SEQ ID NO 10268; 103pp; English.
XX
XX
XX CC The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. AAS64197-AAS94564 represent novel human
XX CC diagnostic coding sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
XX SQ Sequence 502 BP; 111 A; 148 C; 136 G; 107 T; 0 other;
XX
XX
XX Query Match 36.3%; Score 146; DB 23; Length 502;
XX Best Local Similarity 100.0%; Pred. No. 5.3e-32;
XX Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 249 cccctacatgtgtattcagcagccctatgacctgctgagcctgagatggagcaggg 308
XX |||||||
XX DB 353 cccctacatgtgtattcagcagccctatgacctgctgagcctgagatggagcaggg 412
XX
XX QY 309 tagagggaaagtgtacatagacatttccctagagcgaagaattgggggaaagctgtatt 368
XX |||||||
XX DB 413 tagagggaaagtgtacatagacatttccctagagcgaagaattgggggaaagctgtatt 472
XX
XX QY 369 ttatatataaatatcatcagatgta 394
XX |||||||
XX DB 473 ttatatataaatatcatcagatgta 498
XX
XX
XX RESULT 10
XX AAF68420/c

```

XX ID AAF68420 standard; cDNA: 347 BP.
XX AAF68420;
XX 12-APR-2001 (first entry)
XX human lung tumour protein related nucleotide sequence SEQ ID NO:355.
DE human lung tumour protein related nucleotide sequence SEQ ID NO:355.
XX Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
XX lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
XX cytostatic; antisense inhibition; ss.
OS Homo sapiens.
XX W0200100828-A2.
XX 04-JAN-2001.
XX 30-JUN-2000; 2000WO-US18061.
XX 30-JUN-1999; 99US-0346492.
XX 15-OCT-1999; 99US-0419356.
XX 17-DEC-1999; 99US-0468687.
XX 30-DEC-1999; 99US-0476300.
XX 06-MAR-2000; 2000US-0519642.
XX 22-MAR-2000; 2000US-0533077.
XX 10-APR-2000; 2000US-0546259.
XX 27-APR-2000; 2000US-0560406.
XX 05-JUN-2000; 2000US-0589184.
XX (CORI-) CORIXA CORP.
XX Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;
XX Retter MW, Mannion J;
XX WPI: 2001-071488/08.
XX lung tumor-associated proteins and the nucleic acids that encode them,
XX useful for preventing, diagnosing and treating lung cancer -
XX Claim 4; Page 277; 436pp; English.
XX The present invention describes immunogenic portions of lung tumour-
XX associated proteins (I) and the nucleic acids (NAs) that encode them.
XX (I) have cytostatic activity and can be used in gene therapy, antisense
XX inhibition and in vaccines. The NAs and the lung tumour-associated
XX proteins they encode may be used in the prevention, treatment and
XX diagnosis of diseases associated with their inappropriate expression,
XX especially lung cancers. For example, the NAs may be administered to
XX treat diseases by rectifying mutations or deletions in a patient's genome
XX that affect the activity of the protein by expressing inactive proteins
XX or to supplement the patient's own production of (I). Additionally, the
XX NAs may be used to produce the lung-tumour associated protein, according
XX to standard recombinant DNA methodology. Conversely, antisense NA
XX molecules may be administered to down regulate protein expression by
XX binding with the cells own genes and preventing their expression. The NA
XX and complementary sequences may also be used as DNA probes in diagnostic
XX assays to detect and quantitate the presence of similar NA sequences in
XX samples, and hence which patients may be in need of treatment for lung
XX cancer. The (I) may be used as antigens in the production of antibodies
XX and in assays to identify modulators (agonists and antagonists) of the
XX expression and activity of the protein. AAF68083 to AAF68878 and
XX AAF6848 to AAF6878 represent human lung tumour protein related
XX nucleotide and protein sequences which are used in the exemplification
XX of the present invention.
XX Sequence 347 BP; 53 A; 92 C; 127 G; 75 T; 0 other;

QY 52 caggtccctgaagaagctgtgtgacatctgctgtagcagcctaccctccatcagtgaaagca 111
DB 144 CAGGTCCCGCAGAGACTGTGTCATCTGGCTGGACGCTACCTCCATCAGTGAAGCA 85
QY 112 acacccagggcgagcagagaagggctcaggcaccagcaagcaccgcccgcgagga 171
DB 84 ACACCCAGGCGGCGAGGAGNAGGCTCAGGGCAGCAGACACAGCAAGCAGCCCGCGGGA 25
QY 172 tcgataccccaccctccactgg 195
DB 24 TCGATACCCCGACCCCTCCACTGG 1
RESULT 11
AAS32517
ID AAS32517 standard; DNA: 29521 BP.
XX AAS32517;
XX 17-DEC-2001 (first entry)
XX Human genomic DNA for novel endocrine antigen, SEQ ID NO 471.
XX Human; endocrine antigen; ds; cytostatic; antinfertility; antidiabetic;
XX thyroid-active; adrenal-active; androgenic; gastric; gene therapy;
XX antisense therapy; antibody; endocrine cancer; pancreatic disorder;
XX reproductive disorder; endocrine cancer; pancreatic disorder;
XX diabetes mellitus; adrenal gland disorder; hirsutism; thyroid disorder;
XX hyperthyroidism; hypothalamic disorder; vanishing testes syndrome.
XX Homo sapiens.
XX W0200155319-A2.
XX 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US01335.
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 14-AUG-2000; 2000US-0220964.
XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.
XX 14-AUG-2000; 2000US-0225214.
XX 14-AUG-2000; 2000US-0225266.
XX 14-AUG-2000; 2000US-0225267.
XX 14-AUG-2000; 2000US-0225268.
XX 14-AUG-2000; 2000US-0225270.
XX 14-AUG-2000; 2000US-0225447.
XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 18-AUG-2000; 2000US-0226279.
XX 22-AUG-2000; 2000US-0226681.
XX 22-AUG-2000; 2000US-0226868.
XX 22-AUG-2000; 2000US-0227182.
XX 23-AUG-2000; 2000US-0227009.

Query Match 35.4%; Score 142.4; DB 22; Length 347;
Best Local Similarity 99.3%; Pred. No. 4,9e-31;
Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

[illegible]

PR	17-NOV-2000;	2000US-0249211.
PR	17-NOV-2000;	2000US-0249212.
PR	17-NOV-2000;	2000US-0249213.
PR	17-NOV-2000;	2000US-0249214.
PR	17-NOV-2000;	2000US-0249215.
PR	17-NOV-2000;	2000US-0249216.
PR	17-NOV-2000;	2000US-0249217.
PR	17-NOV-2000;	2000US-0249218.
PR	17-NOV-2000;	2000US-0249219.
PR	17-NOV-2000;	2000US-0249225.
PR	17-NOV-2000;	2000US-0249264.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	17-NOV-2000;	2000US-0249300.
PR	17-DEC-2000;	2000US-0250160.
PR	01-DEC-2000;	2000US-0250381.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251038.
PR	05-DEC-2000;	2000US-02516719.
PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251868.
PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2000US-0259687.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-457726/49.

Isolated polypeptide for treating, preventing and prognosing disorders related to the endocrine system including endocrine disorders, reproductive disorders, and gastrointestinal disorders and also for testing and detection e.g. diagnosis -

Disclosure; SEQ ID No 471; 558pp; English.

CC The invention relates to cDNAs encoding novel human endocrine
CC antigens or a fragment having biological activity, a domain, an epitope,
CC full length protein, variant, allelic variant or a species homologue of
CC the cDNA/antigen. The DNAs and polypeptides are useful for preventing,
CC treating or ameliorating a medical condition when administered
CC (e.g. by gene therapy or antisense-therapy). Identifying mutations in
CC the genes coding for the antigens is useful for diagnosing a pathological
CC condition or a susceptibility to a pathological condition. The DNAs,
CC antigens and antibodies raised against the antigens useful for treating,
CC preventing and/or prognosing disorders related to the endocrine system,
CC or hormone imbalance or reproductive disorders, cancers of endocrine
CC tissues, disorders of the pancreas (e.g. diabetes mellitus), the adrenal
CC glands (e.g. hirsutism), ovaries, the thyroid (e.g. hyperthyroidism), the
CC hypothalamus and testes (e.g. vanishing testes syndrome), many examples
CC of diseases and disorders are given in the specification. The present
CC sequence is genomic DNA fragment form a gene encoding an endocrine
CC antigen of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 29521 BP; 6369 A; 8019 C; 7628 G; 7505 T; 0 other;

st Local Similarity 67.28; Pred. No. 2.2e-05;

78; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 7 qcaactgaqctcctaacaaccccccaactgccaccccccaactcccaqgtccctgaagaa 66

PR	17-NOV-2000;	2000US-0249317.
PR	17-NOV-2000;	2000US-0249318.
PR	17-NOV-2000;	2000US-0249324.
PR	17-NOV-2000;	2000US-0249244.
PR	17-NOV-2000;	2000US-0249245.
PR	17-NOV-2000;	2000US-0249264.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	17-NOV-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250160.
PR	01-DEC-2000;	2000US-0250391.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	05-DEC-2000;	2000US-0256719.
PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251868.
PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251889.
PR	08-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.
XX		
PA	(HUMA-)	HUMAN GENOME SCI INC.
XX		
PI	Rosen CA,	Barash SC, Ruben SM;
XX		
DR	WPI; 2001-457726/49.	

PT Isolated polypeptide for treating, preventing and prognosing disorders
PT related to the endocrine system including endocrine disorders,
PT reproductive disorders, and gastrointestinal disorders and also for
PT testing and detection e.g. diagnosis -
XX
XX
XX Disclosure; SEQ ID No 470; 558bp; English.

CC The invention relates to cDNAs encoding novel human endocrine
CC antigens or a fragment having biological activity, a domain, an epitope,
CC full length protein, variant, allelic variant or a species homologue of
CC the cDNA/antigen. The DNAs and polypeptides are useful for preventing,
CC treating or ameliorating a medical condition when administered
CC (e.g. by gene therapy or antisense-therapy). Identifying mutations in
CC the genes coding for the antigens is useful for diagnosing a pathologic
CC condition or a susceptibility to a pathological condition. The DNAs,
CC antigens and antibodies raised against the antigens useful for treating,
CC preventing and/or prognosing disorders related to the endocrine system
CC or hormone imbalance or reproductive disorders, cancers of endocrine
CC tissues, disorders of the pancreas (e.g. diabetes mellitus), the adrenal
CC glands (e.g. hirsutism), ovaries, the thyroid (e.g. hyperthyroidism), the
CC hypothalamus and testes (e.g. vanishing testes syndrome), many examples
CC of diseases and disorders are given in the specification. The present
CC sequence is genomic DNA fragment form a gene encoding an endocrine
CC antigen of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from Wipo at
CC [ftp.wipo.int/pub/published.pct_sequences](http://wipo.int/pub/published.pct_sequences).

Sequence 29543 BP; 6367 A; 8023 C; 7634 G; 7519 T; 0 other;

Query Match	13.7%;	Score 55.2;	DB 22;	Length 29543;
Best Local Similarity	67.2%;	Pred. No. 2.2e-05;		

Qy 7 gcaactgagctcctaaccacccaccactgcaacccaccactccaggtccctgaagaa 66
 || ||| |||| || ||| | | |||| ||| ||||| |||||
 Db 27779 gccactcccgctcctggtccctgacacctgttccatccccaactttgcaggtccctgaagaa 27838

QY 67 gtcgtgtacatctgctgctgacgcctacatcatcagtgaagcaaacccagcg 122
||||| | | ||||| ||||| || | ||||| || ||| | |
Db 27839 gctctggaagctctgtgctgacgcctacatcctcaaatgaagcaaacgccccgg 27894

Db 27839 gtcctggaagctgtgtgctgagcgcctaccttcaaatgaagccacagcccccg 27894

RESULT	13
AAH05343	
ID	AAH05343 standard; cDNA; 560 BP.

AC AAH05343;

DT 26-JUN-2001 (first entry)

DE Human cDNA clone (5'-primer) SEQ ID NO:2178.

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

OS Homo sapiens.
yy

PN EP1074617-A2.
XY

PD 07-FEB-2001.
XX

28-JUL-2000; 2000EP-011612b.
XX

PR	27-AUG-1999	99JP-0300253.
PR	29-JUL-1999	99JP-0248036.

PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.

05 JUN 2000, 200001 024700Z
XX
XX

PA (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Salto K, Yamamoto J;

XX

XX
XX

PT full-length cDNAs defined in the specification, and for the detection

PT XY	full-length cDNAs -
----------	---------------------

PS Claim 1; SEQ ID 2178; 2537pp + CD ROM; English
XY

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification, where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 3602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the protein encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13658 and AAH13659 to AAH18742 represent human cDNA sequences; AA892446 to AAH58963 represent human amino acid sequences; and AAH13632 to AAH13633 represent oligonucleotides, all of which are used in the exemplification of the present invention.

Sequence 560 BP; 125 A; 162 C; 145 G; 124 T; 4 other;

Query Match	11.3%;	Score 45.4;	DB 22;	Length 560;
Best Local Similarity	77.5%;	Pred. No. 0.0032;		
Matches 55; Conservative	0;	Mismatches 16;	Indels 0;	Gaps 0

QY 52 caggtccctgaagaagctctgtgacatctggtgacgcctcctccatcagtgaaagca 111
|||||

Db 434 caggtccctgaagaagctctggaagctgtgctgacgcctacctccacaatgaagcca 493
 QY 112 acaccagcg 122
 494 cagcccccggg 504

RESULT 14
 AAF21845
 ID AAF21845 standard; DNA: 1474 BP.
 XX
 AC AAF21845;
 DT 27-MAR-2001 (first entry)
 DE Human breast and ovarian cancer associated antigen gene SEQ ID 232.
 XX
 KW Human: breast cancer; cytostatic; immunosuppressive;
 KW neutropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 KW antidiabetic; antineoplastic; antitumor; vulnery; immunorepulsant;
 KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KW cardiovascular disorder; wound healing; neurological disease; ds.
 KW
 XX
 OS Homo sapiens.
 PN WO200055173-A1.
 PD 21-SEP-2000.
 PF 08-MAR-2000; 2000WO-US05881.
 PR 12-MAR-1999; 99US-0124270.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM;
 DR WPI: 2000-61515/58.
 DR P-PSDB: AAB58942.

New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases -

Claim 1: Page 656; 1299pp; English.

Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; neuroprotective; antiviral; antiallergic; hepatotropic; antibacterial; antineoplastic; antitumor; vulnery; immunorepulsant; antidiabetic; antineoplastic; antitumor; vulnery; immunorepulsant; antibacterial; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and antagonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemia; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and infectious diseases.

Sequence 1474 BP; 305 A; 458 C; 355 G; 349 T; 7 other;

Query Match 11.3%; Score 45.4; DB 21; Length 1474;
 Best Local Similarity 77.5%; Pred. No. 0.0045;
 Matches 55; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 52 caggtccctgaagaagctctggaagctgtgctgacgcctacctccctcagtggaagcca 111
 809 caggtccctgaagaagctctggaagctgtgctgacgcctacctccacaatgaagcca 868
 Db 112 acaccagcg 122
 869 cagcccccggg 879

RESULT 15
 AAV63641
 ID AAV63641 standard; cDNA: 1686 BP.
 XX
 AC AAV63641;
 DT 15-FEB-1999 (first entry)
 DE Contig 2511785 encoding a human desaturase enzyme.
 XX
 KW Fatty acid; desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome; human;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.
 KW
 XX
 OS Homo sapiens.
 PN WO9846763-A1.
 PD 22-OCT-1998.
 PF 10-APR-1998; 98WO-US07126.
 PR 11-APR-1997; 97US-0834655.
 PA (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;
 DR WPI: 1998-594582/50.
 DR P-PSDB: AAW84154.

New isolated fatty acid desaturase enzymes - used for the production of polyunsaturated fatty acids for use in, e.g. pharmaceutical compositions, nutritional compositions, cosmetics or animal feed

Example 12: Pages 114-115; 165pp; English.

The present sequence encodes a human desaturase enzyme. The sequence was identified based on homology between human cDNA sequences and Mortierella alpina desaturase gene sequences. The specification describes methods for desaturating a fatty acid and for producing a desaturated fatty acid by expressing increased levels of a desaturase. The enzyme can be used for desaturating fatty acids. The enzyme can be used to produce polyunsaturated fatty acids, which can be used for treating malnutrition, in pharmaceutical compositions, in cosmetics or in animal feed. The polyunsaturated fatty acids can be used for treating e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure. They can also be used to inhibit platelet aggregation, cause vasodilation, lower cholesterol levels, inhibit proliferation of vessel wall smooth muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding and other side effects caused by non-steroidal anti-inflammatory drugs, prevent or treat endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral infections, treat AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and

CC inflammatory skin disorders.
XX
SQ Sequence 1686 BP; 322 A; 551 C; 435 G; 378 T; 0 other;

Query Match 11.3%; Score 45.4; DB 19; Length 1686;
Best Local Similarity 77.5%; Pred. No. 0.0048;
Matches 55; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 52 caggtccctgaagaagtctgtgacatctggctggacgcctacctccatcagtgaagca 111
|||||
Db 674 caggtccctgaagaagtctgtgacatctggctggacgcctacctccatcagtgaagca 111
|||||
Qy 112 acaccagagcg 122
||| |
Db 734 cagcccccggg 744

Search completed: October 8, 2002, 03:42:24
Job time: 12284 sec

primer 15
TCGTACCAATCGAAGTCGGAGCGCGCCGACATTTTTTTTTTTTTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector


```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="1686515"
/clone_id="Nc1_CGAP_Brn23"
/tissue_type="glioBlastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT7AD-Pac (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCATTCTGATGTCGGAGGCGCCGCGCATATCTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Scores and M.Fatima Bonaldo."

```

Query Match	85.3%	Score 343	DB 9	Length 482
Best Local Similarity	100.0%	Pred. No. 75-77		
Matches 343	0	Mismatches	0	Gaps 0

OY	52	caggtccctaaagaagctcgtgacatctgctcgagagcctaactccatcaagfyaaagca	111
Db	354	CAGGTCCCTGAAGAAGCTGTGTGACATCTGGCTGGAGCCTACTCCATCATAGTGAAGCA	295
OY	112	acaccacagcgggagagaaaggtctcagggaaccagcaacaaagcaccgccggcgga	171
Db	294	ACACCCAGGCGGCGAGAAAGGCTCAGGGCACCGCAACCAACCCAGCCCGGCGGGA	235
OY	172	tcgataccccaccacctcaccatctgcacagccctgggggctgcacctctcgttact	231
Db	234	TGATACCCCAACCCCTTCATGTGGCAGCCCTGGGGGGTGCCTGCTGCCCTCGGTACT	175
OY	232	gttgtctccctccggccccctcaatgltatctcaagacgcctatggtccttgcttg	291
Db	174	GTTGTCTTCCCTCGGCCCCCTCAAGTGTGATTCACGACGCCCTATGGCCTGTGG	115
OY	292	gccctatggagcaagggtatagaggaagtgagcatalagcacaattctcctaaagcagaat	351
Db	114	GCCCTATGGCAAGGGGTAGAGGGAAGGTGAGCAATTTTCCATAGAGGAGAAAT	55
OY	352	gggggaagcgttatctttatataataatcatcagatgta	394
Db	54	GGGGGAAGCTGTATTTTATTTATTTAAATACATTCAATGTATA	12

RESULT	4
A1133555	
LOCUS	
DEFINITION	A1133555 HA2173 Human fetal liver cDNA library Homo sapiens cDNA, mRNA
ACCESSION	A1133555
VERSION	A1133555.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 561)
AUTHORS	Yu,Y., Zhang,C., Luo,L., Ouyang,S., Li,W., Wu,J., Zhou,S., Liu,M. and He,F. Expression profile analysis of a human fetal liver cDNA library Unpublished (1998) Contact: Yongtao Yu Department of Hematology Beijing Institute of Radiation Medicine 27 Taiping Road, Beijing 100850, P.R.China Tel: 0086-10-68159479 Fax: 0086-10-68214653 Email: yyt4@yahoo.com. Location/Qualifiers
TITLE	
JOURNAL	
COMMENT	
FEATURES	

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source
1. .561
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human fetal liver cDNA library"
/tissue_type="liver"
/dev_stage="fetal"
/lab_host="MC1061/P3"
/note="Vector: pCDNA1"

BASE COUNT      131 a      175 c      147 g      108 t
ORIGIN
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Query Match:	85.3%	Score 343:	DB 9:	Length 561:
Best Local Similarity	100.0%	Pred. No.	7	3e-77:
Matches 343:	Conservative	0:	Mismatches	0:
			Indels	0:
			Gaps	0:

OY	52	caatcccttgaagaagcttgtagcatctgctgtagagcctactccatcaagtgaagga	111
Db	204	CAGTCCCTGAAGAAGTCTGCTGACATCTGGCTGGACCGCTACTCCATCAGTGAAGGA	263
OY	112	aaaccaggcgagagagaaggctcagggaccagcaaccgaagccagcccccggggga	171
Db	264	ACACCAGGCGGGCAGAGAMGGCTCAGGGGCAACGAGAACCAAGCCAGCCCCGGGGGA	323
OY	172	tgcataccccaccacctccatctgcacagccgtgggtgctgcctgctccctctgtact	231
Db	324	TGGATACCCCAACCCCTTCATTTGGGCAGCCCTGGGGGTGGCTGTGCTCCCTCGGTACT	383
OY	232	gttgtctccctccggccccctacaagtgtatcagaagaacctatggccttggctctg	291
Db	384	GTTGTCTTCCCTCCGGCCCCCTCAACATGTGATTCACGACGCCCTATGGCTGTGG	443
OY	292	gacctatggacaagggtcagaagggaagtgagcataltcctlaagcgaagat	351
Db	444	GCCATATGGGACAGGGGTAGAGGGAAAGGTGACATATTTCTTCAAGGAGAAAT	503
OY	352	gggggaagcgttatttttatataaataatcatctcgatgtta	394
Db	504	GGGGGAAGCTGTATTTTATATTAATAATCATTCAATGATTA	546

```

RESULT      5
BG764766
LOCUS
DEFINITION  BG764766             626 bp      mRNA      linear      EST 15-MAY-2001
602736370F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4861600 5',
mRNA sequence.
ACCESSION   BG764766
VERSION     BG764766.1
KEYWORDS    GI:14075419
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 626)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC/DC/DP/
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL),
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNCM1720 row: 1 column: 17
High quality sequence stop: 626.
location/Qualifiers
    1. 626
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:4861600"
FEATURES
    source

```


source 1. 513
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3000629"
/clone_lib="NCI CGAP Lym12"
/tissue_type="lymphoma, follicular mixed small and large cell"
/lab_host="DH10B"
/note="Organ: lymph node; Vector: pCMV-Sport6; Site: 1; SalI; Site 2: NotI; Cloned unidirectionally. Primer: 0.10g dr. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"
BASE COUNT 102 a 141 c 157 g 112 t 1 others
ORIGIN

Query Match 85.1%; Score 342; DB 9; Length 513;
Best Local Similarity 100.0%; Pred. No. 1.3e-76;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 caggtccctgaagaagctgtgacatctgtgacgtgacgtcctacatcagtgaaagca 111
|||||
Db 342 CAGGTCCCTGAAGAAGCTGTGACATCTGTGACGTGACGCTTACCTCATCAGTGAAGCA 283
|||||
QY 112 acaccagcgaggcagagaaggtcaggcaccagcaaccagcccgcgagga 171
|||||
Db 282 ACACCCAGCGGCGGAGAGAGGCTCAGGGCACCAGCAACCAAGCCCGCGCGGA 223
|||||
QY 172 tcgataccccaccctccactgacgtgagctgggtgctgctgctgctgctgact 231
|||||
Db 222 TCGATACCCCAACCCCTCCACTGACGCTGGGGGTGCTGCTGCTGCTGCTGACT 163
|||||
QY 232 gtgtcttccctcggccctccactgacatgtatctcaagcaccatgacctgtgctc 291
|||||
Db 162 GTTGTCTTCCCTCGGCGCCCTCCACTGACATGTGATTCAGCAACCCATAGCTTGGCTGTG 103
|||||
QY 292 gctctatggagcaagggtagaaggaggtgagcatagacatttccctagaacgagaatt 351
|||||
Db 102 GCCGTATGGGACAGGGGTAGAGGAGGATGACATGACATTTTCTTAGAGCGAGAAAT 43
|||||
QY 352 gggggaaagctgtattttatattataataacattcagatgt 393
|||||
Db 42 GGGGGAAGCTGTATTATTATTTAAATACATTCAGATGT 1
|||||

RESULT 8
LOCUS AI279180 431 bp mRNA linear EST 29-JAN-1999
DEFINITION qml8h10.x1 NCI CGAP Lu5 Homo sapiens CDNA clone IMAGE:1882243 3',
mRNA sequence.
ACCESSION AI279180
VERSION AI279180
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 431)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bnrg/image/image.html
Insert Length: 765 Std Error: 0.00

Seq primer: -400P from Gibco.
FEATURES
source 1. 431
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1882243"
/clone_lib="NCI CGAP Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: lung; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from a
neuroendocrine lung carcinoid, and was then primed with a
Not I - 0.10g(dr) primer. Double stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
p773 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 89 a 124 c 129 g 89 t
ORIGIN

Query Match 84.9%; Score 341.4; DB 9; Length 431;
Best Local Similarity 99.7%; Pred. No. 1.7e-76;
Matches 342; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 52 caggtccctgaagaagctgtgacatctgtgacgtgacgtcctacatcagtgaaagca 111
|||||
Db 344 CAGGTCCCTGAAGAAGCTGTGACATCTGTGACGTGACGCTTACCTCATCAGTGAAGCA 285
|||||
QY 112 acaccagcgaggcagagaaggtcaggcaccagcaaccagcccgcgagga 171
|||||
Db 284 ACACCCAGCGGCGGAGAGGCTCAGGGCACCAGCAACCAAGCCCGCGCGGA 225
|||||
QY 172 tcgataccccaccctccactgacgtgagctgggtgctgctgctgctgctgact 231
|||||
Db 224 TCGATACCCCAACCCCTCCACTGACGCTGGGGGTGCTGCTGCTGCTGCTGACT 165
|||||
QY 232 gtgtcttccctcggccctccactgacatgtatctcaagcaccatgacctgtgctc 291
|||||
Db 164 GTTGTCTTCCCTCGGCGCCCTCCACTGACATGTGATTCAGCAACCCATAGCTTGGCTGTG 105
|||||
QY 292 gctctatggagcaagggtagaaggaggtgagcatagacatttccctagaacgagaatt 351
|||||
Db 104 GCCGTATGGGACAGGGGTAGAGGAGGATGACATGACATTTTCTTAGAGCGAGAAAT 45
|||||
QY 352 gggggaaagctgtattttatattataataacattcagatgt 394
|||||
Db 44 GGGGGAAGCTGTATTATTATTTAAATACATTCAGATGTA 2
|||||

RESULT 9
LOCUS AI886741 514 bp mRNA linear EST 21-DEC-1999
DEFINITION wk19f01.x1 NCI CGAP Lym12 Homo sapiens CDNA clone IMAGE:2412793 3',
similar to TR:060426 060426 BC269730_1 ;, mRNA sequence.
ACCESSION AI886741
VERSION AI886741
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 514)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.lnl.gov/db/ftp/image/image.html
Insert Length: 1653 Sld Error: 0.00
Seq primer: -40UP from Glibco
High quality sequence stop: 244.
Location/Qualifiers

FEATURES

source
1. 514

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2412793"
/clone_lib="NCI-CGAP_Lym12"
/tissue_type="Lymphoma, follicular mixed small and large cell"
/lab_host="DH10B"
/note="Organ: Lymph node; Vector: PCMV-SPORT6; Site_1: Salt; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

BASE COUNT 104 a 140 c 160 g 109 t 1 others
ORIGIN

Query Match 84.9%; Score 341.4; DB 9; Length 514;
Best Local Similarity 99.7%; Pred. No. 1.8e-76;

Matches 342; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 52 caggtccctgaagaagctgtgtgaacatctgtgtgacgacctaccatcagtgaaagca 111
DB 343 CAGGTCCCTGAAGAAGTGTGTGACATCTGTGTGACGCGCTACCTCATCAGTGAAGCA 284
QY 112 acaccgaaggcggaagaaggctcaggcgacacgaagcagcccgccggcgga 171
DB 283 ACACCCAGCGGAGAGAGAGGCTCAGGGCACACCAAGCCAGCCCGGGGGGA 224
QY 172 tcgataccccccaccctccactgtgcagcctgtgggtgctgtcctgtcctgtact 231
DB 223 TCGATACCCCCACCCCTCAGTGCAGCGCTGGGGGTGCCCTGCGCTCCTGTACT 164
QY 232 gtgtgttcccttggccctccatcatgtgtattcagcagccctatgtcctgtcgtg 291
DB 163 GTTGTCTCCCTCGGCCCTCCACATGTGTATGAGCGCCCTATGGCCTTGCTCGG 104
QY 292 gctcgtatggacaagggttagaggaagtgagcatagcacatttccttagagcagaatt 351
DB 103 GCCTATGGGACAGGGGTAGAGGAAAGTGAACATATTTCTTCCATGAGCGAATT 44
QY 352 gggggaaagctgtattttatataataacatcagatgta 394
DB 43 GGGGGAAGCTGTATTATTTATATAAATACATTCAGATGTA 1

RESULT 10
AWS18845/c 617 bp mRNA linear EST 03-MAR-2000
LOCUS
DEFINITION ha44e12.x1 NCI-CGAP_Panl Homo sapiens cDNA clone IMAGE:2876590 3'
similar to TR:060426 060426 BC269730.1, mRNA sequence.

ACCESSION
AWS18845
VERSION
AWS18845.1 GI:7156927

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 617)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

TITLE

Unpublished (1997)

JOURNAL

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cgaps-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:

image.lnl.gov/image/html/lresources.shtml
Seq primer: -40UP from Glibco
High quality sequence stop: 378.
Location/Qualifiers

FEATURES

source
1. 617

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2876590"
/clone_lib="NCI-CGAP_Panl"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: PCMV-SPORT6; Site_1: Salt; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

BASE COUNT 123 a 163 c 191 g 140 t
ORIGIN

Query Match 84.9%; Score 341.4; DB 9; Length 617;
Best Local Similarity 99.7%; Pred. No. 1.9e-76;

Matches 342; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 52 caggtccctgaagaagctgtgtgaacatctgtgtgacgacctaccatcagtgaaagca 111
DB 347 CAGGTCCCTGAAGAAGTGTGTGACATCTGTGTGACGCGCTACCTCATCAGTGAAGCA 288
QY 112 acaccgaaggcggaagaaggctcaggcgacacgaagcagcccgccggcgga 171
DB 287 ACACCCAGCGGAGAGAGAGGCTCAGGGCACACCAAGCCAGCCCGGGGGGA 228
QY 172 tcgataccccccaccctccactgtgcagcctgtgggtgctgtcctgtcctgtact 231
DB 227 TTGATACCCCCACCCCTCAGTGCAGCGCTGGGGGTGCCCTGCGCTCCTGTACT 168
QY 232 gtgtgttcccttggccctccatcatgtgtattcagcagccctatgtcctgtcgtg 291
DB 167 GTTGTCTCCCTCGGCCCTCCACATGTGTATGAGCGCCCTATGGCCTTGCTCGG 108
QY 292 gctcgtatggacaagggttagaggaagtgagcatagcacatttccttagagcagaatt 351
DB 107 GCCTATGGGACAGGGGTAGAGGAAAGTGAACATATTTCTTCCATGAGCGAATT 48
QY 352 gggggaaagctgtattttatataataacatcagatgta 394
DB 47 GGGGGAAGCTGTATTATTTATATAAATACATTCAGATGTA 5

RESULT 11
BG231597/c 538 bp mRNA linear EST 09-FEB-2001
LOCUS
DEFINITION naf36e08.x1 Soares_NPBM Homo sapiens cDNA clone IMAGE:4143086 3'
similar to TR:09Y500 Q9Y500 DELTA-6 FATTY ACID DESATURASE. mRNA
sequence.

ACCESSION
BG231597
VERSION
BG231597.1 GI:12726705

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 538)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

TITLE

Unpublished (1997)

JOURNAL

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cgaps-remail.nih.gov
tissue Procurement: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D. and M. Fatima
Bonaldo, Ph.D.

cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNM at:

InfoImage.llnl.gov
Seq primer: -400P from Gibco
High quality sequence stop: 458.

FEATURES

Location/Qualifiers
1..538

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4143086"
/clone_lib="Soares_NPBC"
/tissue_type="Lymphocyte"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pT73D-Pac; Site:1: NotI;
Site:2: EcoRI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGCCGGGTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
is normalized; constructed in the laboratory of M. Bento
Soares (University of Iowa)."

BASE COUNT 106 a 146 c 173 g 113 t
ORIGIN

Query Match 84.8%; Score 341; DB 10; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.3e-76;

Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 52 caggtccctgaagaagctgtgtgacatctgtgtgacgctactccatcagtgaagca 111
DB 341 CAGGTCCCTGAAGAAGCTGTGTGACATCTGTGACGCTACTCCATCATCATGTAAGCA 282
OY 112 acaccagaggggaggaagggctcaggagcaccagcaacagcccgccggcgagga 171
DB 281 ACACCCAGGCGGCGAGAGAGGCTCAGGCGCCAGCAGACCAACGCCCCGGCGGGA 222
OY 172 tcgataccccccccctccactgtgcacagctgggggtgcctgtgcctcctgtgact 231
DB 221 TCGATACCCCCCCTCCTACTGGCCAGCCCGGGGGTGCCTGCTGCTCCCTGGTACT 162
OY 232 gtgtcttccctcggcccccacatgttattcagcagccctatgtgctgtctgtg 291
DB 161 GTTGTCTTCCCTCGGCCCTCATATGTATTACAGAGCCCTATGCGCTCTGG 102
OY 292 gctctatggagcaggggtagagggaggtgagcatagacatttccctagaagcagaatt 351
DB 101 GCCTATGGGACAGGGGTAGAGGGAGGTGAGCATATGTTTCTTCTAGAGCGAAGATT 42
OY 352 gggggaagctgtatttttattataataatcatcagatg 392
DB 41 GGGGGAAGCTGTATTATTTATATTAATAATCATTCAGATG 1
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RESULT 12 642 bp mRNA linear EST 20-OCT-2000
AM005365/wz85h09.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:256565 3'
LOCUS
DEFINITION
ACCESSION AM005365
VERSION AM005365.1 GI:5854143
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 642)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
JOURNAL Unpublished (1998)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNM at:
www.bio.llnl.gov/bbrp/image/image.html
Insert length: 901 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 460.

FEATURES

Location/Qualifiers
1..642

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:256565"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGCCGGGTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 126 a 179 c 197 g 139 t 1 others
ORIGIN

Query Match 84.8%; Score 341; DB 9; Length 642;
Best Local Similarity 99.7%; Pred. No. 2.5e-76;

Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 52 caggtccctgaagaagctgtgtgacatctgtgtgacgctactccatcagtgaagca 111
DB 342 CAGGTCCCTGAAGAAGCTGTGTGACATCTGTGACGCGCTACTCCATCATGTAAGCA 283
OY 112 acaccagaggggaggaagggctcaggagcaccagcaacagcccgccggcgagga 171
DB 282 ACACCCAGGCGGCGAGAGAGGCTCAGGCGCCAGCAGCAACCAAGCCCCGGCGGGA 223
OY 172 tcgataccccccccctccactgtgcacagctgggggtgcctgtgcctcctgtgact 231
DB 222 TCGATACCCCCCCTCCTACTGGCCAGCCCGGGGGTGCCTGCTGCTCCCTGGTACT 163
OY 232 gtgtcttccctcggcccccacatgttattcagcagccctatgtgctgtctgtg 291
DB 162 GTTGTCTTCCCTCGGCCCTCATATGTATTACAGAGCCCTATGCGCTCTGG 103
OY 292 gctctatggagcaggggtagagggaggtgagcatagacatttccctagaagcagaatt 351
DB 102 GCCTATGGGACAGGGGTAGAGGGAGGTGAGCATATGTTTCTTCTAGAGCGAAGATT 43
OY 352 gggggaagctgtatttttattataataatcatcagatg 393
DB 42 GGGGGAAGCTGTATTATTTATATTAATAATCATTCAGATG 1
```

RESULT 13 506 bp mRNA linear EST 30-MAR-1999
A1421947/c
LOCUS
DEFINITION
ACCESSION A1421947
VERSION A1421947.1 GI:4267878
KEYWORDS
EST.

Source	Organism	Human
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
TITLE	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index	
JOURNAL	Unpublished (1998)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapdb-remail.nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.	
FEATURES	CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at: www.bio.lnhi.gov/db/tp/image/image.html Insert Length: 932 Std Error: 0.00 Seq primer: -40UP from Gldpc High quality sequence stop: 255. Location/Qualifiers 1..506 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2099139" /clone_lib="NCI-CGAP_Brn23" /tissue_type="glioblastoma (pooled)" /lab_host="DH10B" /note="Organ: brain; Vector: p7n3-Pac (pharmacia) with a modified polylinker; Site:1: Not I; Site2: Eco RI; 1st strand cDNA was primed with a Not I - Oligo(dT) primer [5'-TGTTCACATCTGAAGTGGAGGCGCGGCATCTCTTTTATTTTTTTTTTTT 3'] ; double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7n3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."	
BASE COUNT	100 a 139 c 159 g 108 t	
ORIGIN		
Query Match	84.7%; Score 340.4; DB 9; Length 506;	
Best Local Similarity	99.7%; Pred. No. 3.3e-76;	
Matches 341; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
QY	52 caggtccctgaagaagctcgtgtgacatcttgcttgagcgcctacctcatagtgaagca	111
DB	342 CAGGTCCCTGAAGAAATCTGTGTGATCTGTGCTGAGACCTCACTCATCAATGAAAGCA	283
QY	112 acacccagcgcgagcagaagaaggtcccaaggacacgaacccaagcccccgcgga	171
DB	282 ACACCCAGCGGCGCAGAGAAGGGCTCAGAGGCACCGACAACCAAGCCGCCGGGGGA	223
QY	172 tcgaatcccccaacctctcaatggtgcacgcctgggggtgacctgctgcctcctgtact	231
DB	222 TCGATATCCCCCACCCCTCCACATGGCGACCGGGGGGTGCCCTGCTCCCTCGTACT	163
QY	232 gtgtcttcacctcgccccctcaatgtgtatctcaagaagcccatgtgctgtgcctg	291
DB	162 GTGTCTTCCCTCGGCCCTCCACATGTGTATTCAGACGACCTATGGCTTGGCTGG	103
QY	292 gctcgtatggagcaggggtgagaggaaggtgacatagacaatttccctagagcgagaatt	351
DB	102 GCCTGATGGGACAGGGGCTGAGAGGAGGTGAGCATACATTTTCTACAGCGGAAATT	43
QY	352 gggggaagctgtatatttatataataatcatcagatct	393
DB	42 GGGGGAAGCTGTATTTTATTTATTTAAATTCATTCAGATGT	1

[illegible]

OY 352 gggggaagctgtatttataataaacattcagatgta 394
 Db 61 GGGGGAAGCTGTATTATTATAATAATACATTGAGATGTA 19

RESULT 15
 AM264721/c 487 bp mRNA linear EST 28-DEC-1999
 LOCUS xq34q01.x1 NCI-CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752513 3
 DEFINITION similar to TR:Q9ZOR9 Q9ZOR9 DELTA-6 FATTY ACID DESATURASE. /; mRNA
 sequence.

ACCESSION AM264721 GI:6641537
 VERSION AM264721.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 487)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov

Tissue Procurement: Chris Moskajuk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
 Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www.bio.lnl.gov/bdrp/image/image.html

Possible reversed clone: polyT not found
 Seq primer: -40UP from Gibco
 High quality sequence stop: 280.

FEATURES
 SOURCE Location/Qualifiers

1..487
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 /db_xref="taxon:9606"
 /clone="IMAGE:2752513"
 /clone_id="NCI-CGAP_Lu28"
 /tissue_type="two pooled squamous cell carcinomas"
 /lab_host="DH10B"
 /note="Organ: lung; Vector: PCMV-SPORT6; site_1: SalI;
 site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies."
 BASE COUNT 95 a 129 c 141 g 120 t 2 others
 ORIGIN

Query Match 83.9%; Score 337.2; DB 9; Length 487;
 Best Local Similarity 98.8%; Pred. No. 2,1e-75;
 Matches 339; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 52 caggccctgaagaagctgtgacatctggtgagcctcactcactcagtgaaagca 111
 Db 366 CAGGTCCCTGAAGAAGTCTGTGACATCTGGCTGAGGCTACCTCATCAGTGAAGCA 307
 OY 112 aacaccaagcgaggaagaaggtcagagcaacagcaagaagccccggcgagga 171
 Db 306 ACACCCAGCGGGCAGAGAGAGGCTCAGGCAACCAAGCAAGCCCCGGCGGGA 247
 OY 172 tggataccccccacccctcactgagccagcctgaggggtgacccctgctgctcctgctact 231
 Db 246 TCGATACCCCCACCCCTCCACTGCGCCAGCCTGGGGTGCCTGCTGCTGCTGCTACT 187
 OY 232 gtgtcttccctcggccccctcacaatgtatcagaagccctatggccttgctcg 291
 Db 186 GTTGTCTTCCCTCGGCCCTCACATGTATTCAGCAGCCCTATGGCCTTGGGCTTGG 127
 OY 292 gcctatgtggaaggtgtagaggaaggtgagcagacatttccctagagcgagaatt 351

Db 126 GCGTGAATGGGACAGGGGCTAAAGGGAAGGTGACCATATTTTCTTAGAGCGGAATT 67
 OY 352 gggggaagctgtatttataataaacattcagatgta 394
 Db 66 GGGGGAAGCTGTATTATTATTATAATAATACATTGAGATGTA 24

Search completed: October 8, 2002, 01:41:20
 Job time: 5371 sec

Tue Oct 8 10:29:06 2002

us-09-806-088-1_copy_18000_18401.rst

Page 10

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2002, 03:43:03 ; Search time 125.54 Seconds
(without alignments)
786.559 Million cell updates/sec

Title: US-09-806-088-1_COPY_18000_18401

Perfect score: 402
Sequence: 1 gatctgcacagcagctctc.....cattcatgattatgag 402

Scoring table:
IDENTITY_NDC
Gapop 10.0 , Gapext 1.0 .

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33.2	8.3	2886	1 US-08-073-383-3	Sequence 3, Appli
2	33.2	8.3	2886	3 US-08-328-239A-2	Sequence 2, Appli
3	33.2	8.3	2886	5 PCT-US94-06365-3	Sequence 3, Appli
4	33.2	8.3	2886	5 PCT-US95-13661-2	Sequence 2, Appli
5	33	8.2	1351	4 US-08-697-954-3	Sequence 3, Appli
6	33	8.2	1872	1 US-08-428-926-1	Sequence 1, Appli
7	33	8.2	1872	1 US-08-435-434-4	Sequence 4, Appli
8	33	8.2	1872	1 US-08-435-436-4	Sequence 4, Appli
9	33	8.2	1872	1 US-08-428-927-1	Sequence 1, Appli
10	33	8.2	1872	1 US-08-428-296-1	Sequence 1, Appli
11	33	8.2	1872	1 US-08-339-517-1	Sequence 1, Appli
12	33	8.2	1872	2 US-08-438-863-4	Sequence 4, Appli
13	33	8.2	1872	2 US-08-438-862-4	Sequence 4, Appli
14	33	8.2	1872	4 US-09-088-435-2	Sequence 2, Appli
15	32.6	8.1	3918	3 US-08-836-329-1	Sequence 1, Appli
16	32.6	8.1	7218	1 US-08-232-463-14	Sequence 14, Appli
17	32	8.0	2808	1 US-08-237-919-1	Sequence 1, Appli
18	32	8.0	2808	4 US-08-732-429-1	Sequence 1, Appli
19	32	8.0	2808	5 PCT-US95-05518-1	Sequence 1, Appli
20	31.8	7.9	1156	2 US-08-984-172-2	Sequence 2, Appli
21	31.8	7.9	2027	1 US-08-150-203A-1	Sequence 1, Appli
22	31.8	7.9	2027	1 US-08-454-730-1	Sequence 1, Appli
23	31.8	7.9	2040	1 US-08-247-475-36	Sequence 36, Appli
24	31.8	7.9	2040	1 US-08-479-650-36	Sequence 36, Appli
25	31.8	7.9	2040	1 US-08-191-866D-57	Sequence 57, Appli
26	31.8	7.9	2040	1 US-08-674-169-36	Sequence 36, Appli
27	31.8	7.9	2040	2 US-08-185-949B-57	Sequence 57, Appli

28	31.8	7.9	4190	4 US-08-924-345-1	Sequence 1, Appli
29	31.8	7.9	8906	2 US-08-826-267-1	Sequence 1, Appli
30	31.8	7.9	15328	2 US-08-888-497-33	Sequence 33, Appli
31	31.8	7.9	15328	4 US-09-362-230-33	Sequence 33, Appli
32	31.8	7.9	15328	5 PCT-US94-07926-33	Sequence 33, Appli
33	31.8	7.9	20235	1 US-07-642-734C-3	Sequence 3, Appli
34	31.8	7.9	20235	3 US-08-439-009A-3	Sequence 3, Appli
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36	31	7.7	152331	3 US-09-128-155-16	Sequence 16, Appli
37	30.8	7.7	152021	3 US-08-922-635-21	Sequence 21, Appli
38	30.6	7.6	3103	3 US-08-826-246-3	Sequence 3, Appli
39	30.6	7.6	3103	3 US-08-944-495-3	Sequence 3, Appli
40	30.6	7.6	3103	3 US-09-126-640-2	Sequence 2, Appli
41	30.6	7.6	3103	4 US-08-925-588-3	Sequence 3, Appli
42	30.6	7.6	3103	4 US-09-288-292A-2	Sequence 2, Appli
43	30.6	7.6	3111	3 US-09-487-444-3	Sequence 3, Appli
44	30.4	7.6	3930	3 US-09-162-373-2	Sequence 2, Appli
45	30.4	7.6	3930	4 US-09-467-946-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-073-383-3
; Sequence 3, Application US/08073383
; Patent No. 5443962
; GENERAL INFORMATION:
; APPLICANT: Draetta, Giulio
; APPLICANT: Cottarel, Guillaume
; APPLICANT: Damaguez, Veronique
; TITLE OF INVENTION: (fillin "Insert title of Application" | ASSAY AND REAGENTS FO
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,383
; FILING DATE: 19930604
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2886 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 73..1773
; US-08-073-383-3

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	Best Local Similarity	47.6%	Pred. No. 1.4			
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Db	194	gtrccctggatgggggggggggggcttctctgcgcggtatcaccaccccttaccacacacatggacg	253			
Qy	114	accacagagcgggacagagaaggggtctcagagagacgaacaaagccccggggagtc	173			
Db	254	accctcggcggggctcggcgaacccgaagccgccttaccacacacttctccctgtcttgcaggggcat	313			
Qy	174	gatacccccaaccctcaacatgagcgaagcttgggggtgtgcccctcgtgcgcctcctgtgactgt	233			
Db	314	ccgagatcttctccctgtctgtctgaaatctctccgaattcttctgaaatgcacagctctctgcacatgatt	373			
Qy	234	tgcttcctcctgtggccccctcacatg	259			
Db	374	cccccaagcccttctggaccccccaatg	399			

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RESULT 2
US-08-328-239A-2
Sequence 2: Application US/08328239A
Patent No. 6037136
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Galatimov, Konstantin
APPLICANT: Jessup, Catherine
TITLE OF INVENTION: Interactions between Raf Proto-Oncogenes
TITLE OF INVENTION: and CDC25 Phosphatases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELLIOT
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(Text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,239A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSV002.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2886 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 73..1773
US-08-328-239A-2

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Query Match	8.3%;	Score 33.2;	DB 3;	Length 2886;
Best Local Similarity	47.6%;	Pred. No. 1.4;		
Matches 98;	Conservative	0;	Mismatches 108;	Indels 0;
Gaps	0;			

[illegible]

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1 RESULT 3
2 PCT-US94-06365-3
3 Sequence 3, Application PC/TUS9406365
4 GENERAL INFORMATION:
5 APPLICANT:
6 TITLE OF INVENTION: Assay and Reagents for Identifying
7 TITLE OF INVENTION: Anti-proliferative Agents
8 NUMBER OF SEQUENCES: 6
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: Floppy disk
11 COMPUTER: IBM PC compatible
12 OPERATING SYSTEM: PC-DOS/MS-DOS
13 SOFTWARE: ASCII (text)
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: PCT/US94/06365
16 FILING DATE: 06-JUN-1994
17 CLASSIFICATION:
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 08/073,383
20 FILING DATE: 04-JUN-1993
21 INFORMATION FOR SEQ ID NO: 3:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 2886 base pairs
24 TYPE: nucleic acid
25 STRANDEDNESS: single
26 TOPOLOGY: linear
27 MOLECULE TYPE: cDNA
28 FEATURE:
29 NAME/KEY: CDS
30 LOCATION: 73..1773
31 PCT-US94-06365-3

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Best Local Similarity	47.6%	Pred. No. 1.4		
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				Gaps 0
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DB	194	ggtccccggatggcggcgccggcttccctgcgcggatcaccacccctcaccacacacatc	253	
QY	114	accacagcggtgcagaaagaggtctcaggtgacaccagaaacccaagcccccgcggatc	173	
DB	254	acctgcgcggggctcggcagaccgcagacggcctgacacacacttccctgtcgcaggagcaat	313	
QY	174	gataccccaccacctcacatctgagcagcctggtgggtgcctctgcgtccctctgtaactgt	233	
DB	314	ccggaaatcttccctctgtgctgaatctctccgaatcttctgatagcactctctgcattgat	373	
QY	234	tgctctccctctggcccccctcaatg	259	
DB	374	cccccaacctcttgagacccccacatg	399	

RESULT 4
PCT-US95-13661-2
; Sequence 2, Application PC/TUS9513661


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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/339517
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 853D4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1872 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-428-926-1

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Matches 75; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 71 ggtgacatctgctgagcgcctaccctccatcagtgaaagcaacacccagcgagagaga 130
Db 536 ggtgacatctgctgagcgcctaccctccatcagtgaaagcaacacccagcgagagaga 130
Qy 131 agggctcagggcagcagcaacacccagcgagagagatcgatccccaccctcc 190
Db 596 tgggcttcggcgagcagaaatgcacagacccacagactgaaatggagaaacccctgg 595
Qy 191 actggcagcctgggggtgcctgc 215
Db 656 actcgtgggcttgccgtgcctgc 680

RESULT 7
US-08-435-434-4
; Sequence 4, Application US/08435434
; Patent No. 5714385
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,434
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
;

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; TELEFAX: 415/952-9881
;
; TELE: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1872 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-435-434-4

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Query Match
Best Local Similarity 8.2%; Score 33; DB 1; Length 1872;
Matches 75; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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Qy 71 ggtgacatctgctgagcgcctaccctccatcagtgaaagcaacacccagcgagagaga 130
Db 536 ggtgacatctgctgagcgcctaccctccatcagtgaaagcaacacccagcgagagaga 130
Qy 131 agggctcagggcagcagcaacacccagcgagagagatcgatccccaccctcc 190
Db 596 tgggcttcggcgagcagaaatgcacagacccacagactgaaatggagaaacccctgg 595
Qy 191 actggcagcctgggggtgcctgc 215
Db 656 actcgtgggcttgccgtgcctgc 680

RESULT 8
US-08-435-436-4
; Sequence 4, Application US/08435436
; Patent No. 5721139
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,436
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1872 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-435-436-4

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Db 596 TGGGCTTCGGCGCAGCAGAAAGATGTCAGAGACCCGAGACTGAAGATGGAGACCCCTGG 655

Oy 191 actggccagcgtgggggtgacctgc 215

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1 RESULT 10
2 US-08-428-298-1
3 : Sequence 1, Application US/08428298
4 : Patent No. 5763213
5 :
6 : GENERAL INFORMATION:
7 :
8 : APPLICANT: HO, Wei-Hsien
9 : APPLICANT: Osheroff, Phyllis I.
10 : TITLE OF INVENTION: SENSOR AND MOTOR NEURON DERIVED FACTOR (SMDF)
11 : NUMBER OF SEQUENCES: 5
12

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RESULT 10
 US-08-428-298-1
 ; Sequence 1, Application US/08428298
 ; Patent No. 5763213
 ; GENERAL INFORMATION:
 ; APPLICANT: Ho, Wei-Hsien
 ; APPLICANT: Osheroff, Phyllis L.
 ; TITLE OF INVENTION: SENSOR AND MOTOR NEURON DERIVED FACTOR (SMDF)
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible

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/ IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
;

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SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08
FILING DATE: 25-APR-1995

CLASSI

;
PRIOR AP

APPLICATION NUMBER: 14-NOV-14

ATTORNEY/AGENT INFORMATION:
FILING DATE: 14-NOV-1994

NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 00,000

REFERENCE/DOCKET NUMBER: 853D2
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION: 415/225-1994
TELEPHONE: 415/225-1994
; ;
; ;

TELEFAX: 415/952-9881

TELEX: 910/371-7168

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; INFORMATION FOR SEQ ID NO: 1:
:
: SEQUENCE CHARACTERISTICS:

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SEQUENCE CHARACTERISTICS:
LENGTH: 1872 bases

TYPE: nucleic acid

STRANDEDNESS: single

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;          TOPOLOGY: linear
MS-08-A28-298-1

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T-067-074-00-50

Query Match	8.28;
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Best Local Similarity 51.7%;
Matches 75. Conservative

matches 10; conservative

QY 71 ggtgacatctgctgacgccta

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D6 536 GGTCCGCCGCCGAGAGGTCCTCCA

131 aagagctcaagagcaccgaagcga

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Db 596 TGGGCTTCGGCAGCAGAAGACA

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[illegible]

Db 656 ACTCGTGGGCTGGCCGTGCCCT

RESULT 11

REC'D 11
US-08-339-517-1

; Sequence 1, Application US/0833

; Patent No. 5770567

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GENERAL INFORMATION:
APPLICANT: Ho, Wei-Hsien
APPLICANT: Osherooff, Phyllis L.
TITLE OF INVENTION: SENSOR AND MOTOR NEURON DERIVED FACTOR (SMDF)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,517
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-339-517-1

Query Match      8.2%; Score 33; DB 1; Length 1872;
Best Local Similarity 51.7%; Pred.No.1.3;
Matches 75; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY   71 ggtgacatcttgcttgaagcctacctcatcgtagaaccaaccacaggcgggagaga 130
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DB   536 gctgcgcgcgcgcgagaggtctctccagcccccttcactagctgagtgcagaccattcttta 595
QY   131 agggctcagcgaccacccaacgaagcagcccgcggcgagatcatatacccccctcc 190
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB   596 tgggcctccggcagcagagagacatgcacagaccgccagactgaagatggagaaacccctgg 655
QY   191 actygcacgcttgygggtgcctgc 215
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DB   656 actcgtgggcctggccctgcctgc 680

RESULT 12
US-08-438-863-4
Sequence 4, Application US/0843863
Patent No. 5849585
GENERAL INFORMATION:
APPLICANT: Matthew, Jennie P.
APPLICANT: Ronghao Li
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California

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? COUNTRY: USA
? ZIP: 94080
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: patin (Genentech)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/438,863
? FILING DATE: 10-MAY-1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Lee, Wendy M.
? REGISTRATION NUMBER: 00,000
? REFERENCE/DOCKET NUMBER: 946
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415/225-1994
? TELEFAX: 415/952-9881
? TELEX: 910/371-7168
? INFORMATION FOR SEQ ID NO: 4:
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? STRANDEDNESS: single
? TOPOLOGY: linear
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US-08-438-863-4
?
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Best Local Similarity 51.7%; Pred. No. 1.3; Mismatches 70; Indels 0; Gaps 0
Matches 75; Conservative
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Oy 71 ggtacatcggctgagcgccctaactcatcagtgaaggcaaccaccagcggcgagaga 130
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Oy 131 agggctaacggacacccagcaacgaagcccccggggatgataccccaccctcc 190
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Db 656 ACTGtGtGgCCTGgCGGTGCCCTGC 680
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RESULT 13
US-08-438-862-4
? Sequence 4, Application US/08438862
? Patent No. 6033660
? GENERAL INFORMATION:
? APPLICANT: Mather, Jennie P.
? APPLICANT: Li, Ronghao
? APPLICANT: Chen, Jian
? TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
? NUMBER OF SEQUENCES: 9
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Genentech, Inc.
? STREET: 460 Point San Bruno Blvd
? CITY: South San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94080
?
COMPUTER READABLE FORM:
? MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: patin (Genentech)*
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/438,862
? FILING DATE: 10-MAY-1995
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-438-862-4

Query Match 8.28; Score 33; DB 3; Length 1872;
Best Local Similarity 51.7%; Pred. No. 1.3;
Matches 75; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 71 ggtgacatctgctggagcctactcatagtgaggaacacccagcgcgagaga 130
Db 536 ggtgacatctgctggagcctactcatagtgaggaacacccagcgcgagaga 130
Qy 131 agggctcaggagcagcaacagcagcccgcgagcgatgataccacacccctcc 190
Db 596 tgggttcggcgagcagcaacagcagcccgcgagcgatgataccacacccctcc 190
Qy 191 actggcagcctggggggtgccttc 215
Db 656 actggtggcctggcgccgctgccttc 680

RESULT 14

US-09-088-435-2/c
Sequence 2, Application US/09088435
Patent No. 6277619

GENERAL INFORMATION:

APPLICANT: LAU, PREETI
APPLICANT: CORLEY, NEIL C.
APPLICANT: GUEBLER, KARL J.
APPLICANT: PATTERSON, CHANDRA
TITLE OF INVENTION: SERINE DEHYDRATASE HOMOLOG
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0512 US
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1485 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: THPLAZS08
US-09-088-435-2

Query Match 8.1%; Score 32.6; DB 4; Length 1485;
Best Local Similarity 49.7%; Pred. No. 1.6;
Matches 83; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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Qy 110 caaacccagcgcgagcagagaaggtcagggcaccagcaacccaagcccgcgcg 169
Db 839 caccaccccgccagcagacccccccacccacccacccacccacccacccacccaccc 780
Qy 170 gatgatacccccacccctcactgagcagcctggggggtgcctgc 216
Db 779 cctcagcactgcttttgccttgcacacagcagcgtggcctgcttgc 733

RESULT 15

US-08-836-329-1
Sequence 1, Application US/08836329
Patent No. 6090546

GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: Method for the Detection of Ras Oncogenes,
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,329
FILING DATE:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: 825..947
FEATURE:
NAME/KEY: exon
LOCATION: 1388..1567
FEATURE:
NAME/KEY: exon
LOCATION: 2118..2278
FEATURE:
NAME/KEY: exon
LOCATION: 3034..3158
FEATURE:
NAME/KEY: exon
LOCATION: 3459..3616

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2002, 03:36:27 ; Search time 6458.34 Seconds
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Gap 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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33: em_hvggo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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16	539.2	31.7	1498	5	AB074149	AB074149 Oncorhynch
17	535.2	31.5	1692	5	AB070444	AB070444 Oncorhynch
18	529	31.1	1590	5	AF309556	AF309556 Dario rer
19	517.4	30.4	3408	10	AB072976	AB072976 Mus muscu
20	517.4	30.4	3415	10	BC022139	BC022139 Mus muscu
21	504	29.6	1790	5	AF309557	AF309557 Cyprinus
22	503.8	29.6	3380	10	AB052085	AB052085 Rattus no
23	497.8	29.3	2621	9	HSMB00210	HSMB00210 Rattus no
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28	492	28.9	4213	9	HSMB002921	HSMB002921 Homo sapi
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ALIGNMENTS

RESULT	1	LOCUS	AF134404	DEFINITION	Homo sapiens delta-6 fatty acid desaturase (CYP5BP) mRNA, complete cds.	ACCESSION	AF134404	VERSION	AF134404.1	GI:4868365	ORGANISM	human.	REFERENCE	1 (bases 1 to 1705)	TITLE	Human retina-specific delta 6 fatty acid desaturase	AUTHORS	Ll.W., Metzker,M.L., Caskey,C.T. and Petrukhin,K.	JOURNAL	Unpublished	REFERENCE	2 (bases 1 to 1705)	TITLE	Direct Submission	AUTHORS	Ll.W., Metzker,M.L., Caskey,C.T. and Petrukhin,K.	JOURNAL	Submitted (11-MAR-1999) Human Genetics, Merck Research Laboratories, P.O. Box 4, West Point, PA 19486, USA	FEATURES	Location/Qualifiers	Source	1..1705
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71..1408
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/codon_start=1
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/protein_id="AAD31282.1"
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/translation="MGSVGEPEPREGPAPCAPLPTECWEQIRAHDPGRKMLVIERR
VYDISRMAQRHPGGSRLIGHGADADARAFKQDLPVRFKLPDILLIGLPEPES
QDGPLNQLVEDPFRALHQAAEDMKLPASPFPAFLIGHILLAMLVAMLLIYLGPDM
VPSLAAPFLIASOASMCLOHDHGIASIKRSMNVNAQKFNVGOLKGSAMHMR
HFOHAKPNIEHNDPDYTVAPVFLIGSSVYKRRRYLYNOOHLYPLIDPILLT
LVNFEVENLALMYCMQMDILMASTYARFLSYLPFYGPVYLFFVAVRLESIM
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RESULT 2 BC004901 1816 bp mRNA linear PRI 12-JUL-2001
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SOURCE human.
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Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1816)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
Contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Kettelman and Anuradha Madan
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAL Plate: 11 Row: b Column: 11
This clone was selected for full length sequencing because it
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Query Match 99.9%; Score 1698.4; DB 9; Length 1816;
Best Local Similarity 99.9%; Pred. No. 5.5e-288;
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LOCUS
DEFINITION Sequence 3 from Patent EPI035207.
ACCESSION AX035942
VERSION AX035942.1 GI:1191484
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1757)
AUTHORS Marguardt, A. and Weber, B. H.
TITLE Cna molecules of the members of gene family encoding human fatty
JOURNAL acid desaturases and their use in diagnosis and therapy
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ORIGIN

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VERSION	AF084560.1	GI:10798852	
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SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 1757)		
AUTHORS	Marquardt,A., Stohr,H., White,K. and Weber,B.H.F.		
TITLE	cDNA cloning, genomic structure, and chromosomal localisation of three members of the human fatty acid desaturase family		
JOURNAL	Genomics 66 (2), 175-183 (2000)		
MEDLINE	20318619		
PUBMED	10860662		
REFERENCE	2 (bases 1 to 1757)		
AUTHORS	Marquardt,A., Stoehr,H., Passmore,L.A., Kraemer,F., Rivera,A. and Weber,B.H.F.		
TITLE	Direct Submission		
JOURNAL	Submitted (05-AUG-1998) Institute of Human Genetics, University of Wuerzburg, Biozentrum, Am Hubland, Wuerzburg D-97074, Germany		
FEATURES	Location/Qualifiers		
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QY	155	cgcgcgcacgcacccacccgcgcgcgaagaatgctgtgcatcagagcgcgcgtactagaatc	214
Db	229	CAGAAAGCATTAACCTGGCGACCGAGAGGTGGCTGGTATTGACCGCAAGGTTTACAAATC	288
QY	215	agccgcgtggcaacagcgggaaccacggggggagagcgccctactgagccacagcgcgtgag	274
Db	289	ACCAAATATGCTCATTCACGACACCCTGGGGGGCCACCGGTGTATGGGGCATTAAGGTGGAGAA	348
QY	275	gaacgcacagatgacctcgtgacctcaatcaagaatcattttgttgcaagtctccta	334
Db	349	GATGCAACGAGATGCTTCCTCCGGCCCTTCACCCCTGACCTCGAAATTCGTGGGCAAGTCTTG	408
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Db	409	AAACCCCTGTGATTTGGTGGAACTGGCCCCGGAGAGGCCAGCGAGGACACGCGCAAGAAC	468
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QY	455	gattgcagatcccaacctcttcgtcttcctactatgvgacacatcctcgtgcattgtagagtgtg	514
Db	529	AAGACCAACACAGTGTCTTCCTCCTCCTCCTCGGCCACACATCATACGCCCTGGAGACATT	588
QY	515	gactgtgtccttatctactacctctggtctcgtgcgcgtgggtgtgccagttgcctcgcgcgttc	574
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QY	635	aacttcagaagaatcctgttggaacaacgttgcgcagaagaattcgtgatggggcagctaaag	694
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QY	695	gagcttcctgcgcacatcgtgtgaacttcgcgcacattccagcaacgcgcaagcccaatc	754
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QY	812	gtcagatattgacaagaagaacacagatalactaccctctacaacacagacaccttgatttc	871
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QY	1172	gagccctcaacttttaccacacttgggttggcgggaccccaacttccagatcgaagacac	1231
Db	1249	GAGCAGTCTTTTAAAGACTGTGTTCAGTGTGACACTTAACTTCCAAATTGAGACACAC	1308
QY	1232	cctctcccccagagtagtcgagacacacactacagccgggtgtgcccgcgtgtctcaagtgcgtg	1291
Db	1309	CTCTTCCCAACATGCCCCCGGACCAACTTATACAAAGATGCCCCCTGTGTGAAGTCTATA	1368
QY	1292	tgttcgaagcaagcgtctcagctcagctagaagtgtgaagccctctctcaacgcgcgtgtgtgacac	1351
Db	1369	TGTGGCAACCAATGCGCTTGTAATTAACCAAGGAAAGCCGCTACTAAGGGCCCTGCTGGACATC	1428
QY	1352	gtcaggtcccttgaagaagatctgtgtgacatctgtctgagacgctactccatcaagtgaag	1411
Db	1429	ATCAGGTCCCTGAAAGAAAGTGTGGAAAGCTGTGGCTGAGCGCTACTACTTACAAATGAAGC	1488
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JOURNAL		<p>AX035941 9</p> <p>AX035941 2 from Patent EP1035207.</p> <p>AX035941</p> <p>AX035941.1 GI:1191483</p> <p>unidentified.</p> <p>unidentified.</p> <p>unclassified.</p> <p>1 (bases 1 to 4089)</p> <p>Marquardt, A. and Weber, B.H.</p> <p>Cdna molecules of the members of gene family encoding human fatty acid desaturases and their use in diagnosis and therapy</p> <p>Patent: EP 1035207-A 2 13-SEP-2000;</p> <p>MULTIGENE BIOTECH GMBH (DE)</p>			
AUTHORS					
TITLE					
REFERENCE					
LOCUS					
DEFINITION					
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VERSION					
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OY	455	gaatgccagtcceacactctcttgccttctcctacatcgycgaatcctc	gtgcataagtagtgcgt	514	
Db	453	AAAAACCAACACCTGTTCTTCCTTCCTCTGCTCCACATCATCTCTGAAGAAAGCCTT		512	
OY	515	gcctcgagccctatctacccctccgtggtccctcgagctgtgctccgaagtgcctgcgcgcttc		574	
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OY	575	atccctgscalccttcacgagctcagctcagctctgtctgtctcagacatgac	cttgycacatgc	634	
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QY	1292	tgttcgaagcagcgccctcaagctcagctagaagaatgaaagcccttcctcaacgagctgtgtgacatc	1351
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VERSION	AX253297.1		GI:16073841
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ORGANISM	Rattus sp.		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
	Rattus.		
REFERENCE	1 (bases 1 to 1335)		
AUTHORS	Wither, M.D., Smith, H.L., Allen, S.J., Ponton, A. and de Antueno, R.J.		
TITLE	Polynucleotides that control delta-6-desaturase genes and methods		
JOURNAL	Patent: WO 0170993-A 3 27-SEP-2001;		
SCOTIA Holdings PLC (GB)			
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Db	79	cagagagcacaacacctgcgcacacgcgagggggtcgtcatcgaacggaaagctcacaactt	138
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QY	335	cagccctgttgatctgagagagctgtgtcctcgggaagacccagacccaagatcagccctgag	394
Db	259	aagcccttgatctgagagagctgtgtcctcgggaagacccagacccaagatcagccctgag	318
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Db	319	tctcagatcaccgagagacttcgagcctctgcacacacagcgacgcgagagacatgaagctgttc	378
QY	455	gatgcagctccacacttctgtccttactagtggtgcacatccctgtgcagatggaggtgtgtg	514

Db	379	AAAACCAACCACTGTTCTTCTTCTTCTCCCTCCCTGTCACATATGTCATGGAAGATC	438
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Qy	575	atctggccatctctcgaagctgaagtcgtgtgtctgcagaatgaacttggccatgcttc	634
Db	499	GTCCTTGCTACCTCCAGGCCACAGCTGGATGGCTACCAACATGATTTATGGCACTTTCT	558
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Qy	695	ggcttcctccgcccactgtgtggaacttcgcgcacttcacagcacaacgcaccaacacac	754
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Qy	755	ttccacaaagaacccaagaagtcgaagtcgtgcgcgcgtcttcctcttggggagtc---catc	811
Db	679	TTTCCACAAAGACCCCGACATTAAGAGCCCTGCACGTGTTTGCCCTTGCAAGTGGACGCC	738
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Db	859	ATGATCAGACGACGAGACTGGGTGACTTGGCTTGCCATCAGTACATCATCAGCTTTC	918
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Qy	1292	tgtgccaagcacgagcctcaagctacgaagtcgaagcccttctcactcaacgcgctgtgtgacac	1351
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DEFINITION	Sequence 4 from Patent WO0170993.	Linear	PAT 10-OCT-2001
ACCESSION	AX253298		
VERSION	AX253298.1	GI:16073842	
KEYWORDS	human.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

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Db	859	ATGATCGTCCATTAAGAACTGGGCTGGACCTGGCCCTGAGCTACTACATCCGGTTC	918
Qy	992	ttctatcttcaactccctctctcaaggcgctccctgggggtgctctctcttctgtctgc	1051
Db	919	TTTCATCACCTACATCCCTTTCTACGGCAATCCGGAAGCCCTCTTTTCTCAACTTCATC	978
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Db	1039	ATTGACACGAGAGGCGCTACCGGTGACTGGTTTCAATAGACACAGCTGACAGCCACTGCAACGNG	1098
Qy	1172	gagccctcaacttttaccacactggttctcagcggagaccctcaacttccaatgtgaagaccac	1231
Db	1099	GAGCAGTCCCTTCTTCAACGACACTGTTTCACTAGTGACACCTTAATCTTCAGATTTGAGCACAC	1158
Qy	1232	ctcttcccccagatgctcgagacacacacacagccgggtgtggcccgctgtgtaagctgcg	1291
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QY	703	cgcccaactgtatggaacttcgcgcaacttcgaagcaacagcccaagcccaacttcacaa	762		
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QY	763	agaaccaagctgaacgcttgycgcgcgccttcctccctcggggga---gtactcgtagta	819		
DB	630	GGATCCGATGTGAACATATGCTGCACGTTGTTGTTGGGGAAATGGCACCCATGAGTA	689		
QY	820	tgycgaagaagaagcagatatacctacctaacaacagcagcaaccttactcttcctgat	879		
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QY	940	gtgcattgagtgagcggaattgtctctggygcgcgacgtctctatgcccgtcttcttatc	999		
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DB	870	CTACATCCCTTTCTACGGCATCCGAGGCCCTCTTTTCTCTCAACTTATATAGGTTCT	929		
QY	1060	ggaagaaccactggtctgttgaatcacacagatglaaaccaatcccaagaagaatcgcga	1119		
DB	930	GGAGAGCCACGTGTTGTGTGGGTGCACACAGATGAMTCAACATGTCATGTGAGATTGACA	989		
QY	1120	cgaagaagcaaccggaactggtgtcaagctctcaagctgtgcagccactgcacgctgagccctc	1179		
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DEFINITION	Oncorhynchus mykiss putative delta 6-desaturase (FDb) mRNA,		
ACCESSION	AF301910		
VERSION	AF301910.1	GI:13447754	
KEYWORDS			
SOURCE	Rainbow trout.		
ORGANISM	Oncorhynchus mykiss		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Actinopterygii; Neopterygii; Telostei; Euteleostei;		
TITLE	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.		
JOURNAL	1 (bases 1 to 1866)		
AUTHORS	Sellier, I., Panserat, S., Kaushik, S. and Bergot, P.		
REFERENCE	Cloning, tissue distribution and nutritional regulation of a		
AUTHORS	delta-6-desaturase-like enzyme in rainbow trout		
TITLE	Comp. Biochem. Physiol., B 130, 83-93 (2001)		
JOURNAL	2 (bases 1 to 1866)		
AUTHORS	Sellier, I., Panserat, S., Kaushik, S. and Bergot, P.		
TITLE	Direct Submission		
JOURNAL	Submitted (30-AUG-2000) Fish Nutrition Laboratory, INRA,		
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Search completed: October 8, 2002, 03:36:51
Job time: 12262 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2002, 03:42:24 ; Search time 648.94 Seconds

(without alignments)
4497.726 Million cell updates/sec

Title: US-09-806-088-2
Perfect score: 1700
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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[Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1700	100.0	1700	21	AAZ93706
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4	1443.8	84.9	1663	23	AAH7448
5	1373	80.8	1478	19	AAV34206
6	1122.6	66.0	1810	23	AAV34206
7	924.2	54.4	2016	19	AAV34206
8	699.4	41.1	3083	22	AAV34206
9	699.4	41.1	3106	21	AAV34206

10	699.4	41.1	4089	21	AAH90953	Human fatty acid d
11	697.8	41.0	1335	22	AAI66599	Rat fatty acid des
12	697.8	41.0	3184	21	AAZ48247	Human oxidoreducta
13	696.2	41.0	1335	22	AAI19403	Rat delta-6-desatu
14	694.6	40.9	1335	22	AAI19403	Human delta-6-desa
15	607.4	35.7	2825	22	AAH4377	Human full-length
16	590.2	34.7	2257	19	AAH63643	Contig 253538a enc
17	590.2	34.7	2257	20	AAH00910	Human desaturase g
18	590.2	34.7	2257	20	AAH2642	Contig 253538a enc
19	590.2	34.7	2257	21	AAH4939	Human delta-5-desa
20	590.2	34.7	2257	21	AAH09453	Human contig 2535
21	590.2	34.7	2257	21	AAH14594	Nucleotide sequenc
22	492.8	29.0	1856	22	AAH15766	Human CDNA sequenc
23	492	28.9	2236	22	AAH94234	Human full-length
24	492	28.9	2614	21	AAH76207	Human ORF ORF1762
25	492	28.9	4203	21	AAH09955	Human fatty acid d
26	492	28.9	4205	21	AAH09952	Human fatty acid d
27	490.4	28.8	1946	22	AAH17649	Human CDNA sequenc
28	488.8	28.8	2080	22	AAH4270	Human full-length
29	488.2	28.7	1335	21	AAH4932	Human delta-5-desa
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31	487.8	28.7	2558	22	AAH94786	Human full-length
32	484	28.5	1843	19	AAH63642	Contig 2535 encodi
33	484	28.5	1843	20	AAH0909	Human desaturase g
34	484	28.5	1843	20	AAH2641	Contig 2535 encodi
35	484	28.5	1843	21	AAH4938	Human delta-5-desa
36	484	28.5	1843	21	AAH09452	Human contig DNA e
37	484	28.5	1843	21	AAH14593	Nucleotide sequenc
38	483.8	28.5	2629	22	AAH9666	Human proteinenco
39	477.4	28.1	1474	21	AAH21845	Human breast and o
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41	419.2	24.7	1686	20	AAH00908	Human desaturase g
42	419.2	24.7	1686	20	AAH2640	Contig 2511785 enc
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45	419.2	24.7	1686	21	AAH14592	Nucleotide sequenc

ALIGNMENTS

RESULT 1	
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AC	16-AUG-2000 (first entry)
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DE	CYB5RP fatty acid desaturase CDNA.
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KW	CYB5RP; fatty acid desaturase; cytochrome b5; macular degeneration;
KW	skin disease; diabetes; inflammation; autoimmune disease;
KW	cardiovascular disease; viral infection; virus; identification;
XX	human; ss.
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PD	20-APR-2000.
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PE	05-OCT-1999; 99WO-US23253.
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PR	09-OCT-1998; 98US-0103760.
XX	
PA	(MERI) MERCK & CO INC.
XX	

PI Petrunkin K, Caskey CT;
XX WPI: 2000-317847/27.
DR P-PSDB; AAY83229.
XX
PT Novel cytochrome b5-related protein useful for identifying modulators
PT useful for treating retinal dysfunction such as macular degeneration,
PT skin diseases, diabetic complications and cardiovascular disorders
XX
XX Claim 2; Figure 3; 44p; English.
CC CYB5RP is a fatty acid desaturase and a cytochrome b5-related protein.
CC Pharmaceutical compositions comprising an activator or an inhibitor of
CC CYB5RP protein are useful for treating macular degeneration. The
CC CYB5RP protein is useful for identifying its activators or inhibitors
CC which are useful for treating abnormal conditions associated with
CC CYB5RP protein activity such as skin disease, diabetic complications,
CC inflammatory and autoimmune disorders, cardiovascular disorders and
CC complications of viral infection. Large amounts of valuable essential
CC fatty acids can be produced by the expression of CYB5RP protein.
XX
SQ Sequence 1700 BP; 319 A; 560 C; 480 G; 341 T; 0 other;

Query Match 100.0%; Score 1700; DB 21; Length 1700;
Best Local Similarity 100.0%; Pred. No. 0;
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Db 1201 cgggacatccaactccagatcagagacacacccctctcccaagatgacgagacacaa 1260
QY 1261 cagccgggtggcccgctgtgtcaagctgtgtgccaagagacagccctcagatcgaagt 1320
Db 1261 cagccgggtggcccgctgtgtcaagctgtgtgccaagagacagccctcagatcgaagt 1320
QY 1321 gaaagcccttcctcaacgcgcgtgtgtgagatcgtcaggtccctgaaagaagctgtgacat 1380
Db 1321 gaaagcccttcctcaacgcgcgtgtgtgagatcgtcaggtccctgaaagaagctgtgacat 1380
QY 1381 ctggtctgagacgtctcctccatcagtgaaagcaacacccagcggtgcagagaaggtctca 1440
Db 1381 ctggtctgagacgtctcctccatcagtgaaagcaacacccagcggtgcagagaaggtctca 1440
QY 1441 gggcaccagcaacacagacagaccccccggcgagatcagatacccccccctccacttgcca 1500
Db 1441 gggcaccagcaacacagacagaccccccggcgagatcagatacccccccctccacttgcca 1500
QY 1501 gctctgggtgtgaactgctgcctcctctgtgactgtgtctccctcggcccccctacat 1560
Db 1501 gctctgggtgtgaactgctgcctcctctgtgactgtgtctccctcggcccccctacat 1560
QY 1561 gttgattgaagacccctatgcttctgtgtcctggtcctgagatgagacagaggtagaag 1620
Db 1561 gttgattgaagacccctatgcttctgtgtcctggtcctgagatgagacagaggtagaag 1620
QY 1621 gtgagacagacatcttccctagaagcagaatgtgggggaaagcgttatattatataa 1680
Db 1621 gtgagacagacatcttccctagaagcagaatgtgggggaaagcgttatattatataa 1680
QY 1681 aatacatcagatgtaaaa 1700
Db 1681 aatacatcagatgtaaaa 1700

RESULT 2

AAH99727/c
ID AAH99727 standard; cDNA; 1772 BP.
XX
AC AAH99727;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human protein encoding cDNA sequence SEQ ID NO:562.
XX
KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW antibacterial; endocrine; cardiac; central nervous system; virucide;
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW antiagregant; haemostatic; vulnery; antilicer; osteopathic; eczema;
KW dermatological; antiallergic; antiaslamic; antidiabetic; cytostatic;
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder; ss.
XX
OS Homo sapiens.
XX
PN M0200153455-A2.
XX
PD 26-JUL-2001.
XX
PF 22-DEC-2000; 2000MO-US35017.
XX
PR 23-DEC-1999; 99QS-0471275-
PR 21-JAN-2000; 2000HS-0488725.
PR 25-APR-2000; 2000HS-0552317.
XX
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR MPI: 2001-457603/49.
XX
DR P-PSDB; AAM25786.
XX
PT Isolated human polynucleotides encoding polypeptides, useful for the
XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
XX
PS Claim 1; Page 608-609; 1217pp; English.
XX
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiac;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianaemic; antiagregant; haemostatic; vulnery;
CC antilicer; osteopathic; dermatological; antiallergic; antiaslamic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
XX neurological disorders.
XX
SQ Sequence 1772 BP; 342 A; 518 C; 582 G; 330 T; 0 other;

Query Match 99.9%; Score 1698.4; DB 22; Length 1772;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1699; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ctcgcttcctcggggtctgtctcgcacccgcgcgttgatcccaagactcg 60
DB 1707 GTTCGCTTCCTCGGGGCTTGTCTCGGACCTCGGACCCGCTGGATCCCAAGACTCG 1648
QY 61 tgcgtgcagcatggcggtcgcggagccggagccggagggagccggcgagccggg 120
DB 1647 TCGGTGCAGCANTGGCGGCGGTGGGAGCCGGACCCGGAGGAGACCCGGCGAGCGGG 1588
QY 121 ggcacgcgtgcggcactctgtctggagagagatccgcgcgcagccagccgcgcgacaa 180
DB 1587 GGCACCGGTGCCACCTTCGTGTGGAGACAGATCCGCCGACACGACGCCGGCGACAA 1528
QY 181 gtgctgtcatcagagcgcgctcagacatcagccgctgggcagagcgagccagc 240
DB 1527 GTGGCTGTGTCATCGAGCGCGCGCTTACGACATCGCCGCTGGGCAAGCGGACCCAGG 1468
QY 241 gggcagcgccctcatcgcgcacccagcgctgagagagcgacgagcttcgcttc 300
DB 1467 GGGCAGCGCCTCATCGGCGCACCGCGCTGAGAGACCGACGATGCTTCCTGCTT 1408
QY 301 ccataagatctcaatttctgagcaagttcctacagccctgtgaltgagagactgagc 360
DB 1407 CCATCAGATGTCATATTTTGTGCGCAAGTTCCTACAGCCCGCTGTGATTTGAGAGACTGCGC 1348
QY 361 tccggaagaaccagccagagatgagacccctgaatgcgagctgtctgagagactccgagc 420
DB 1347 TCCGGAAGAACCACCGACGAGATGACCCCTGATCGAGTGGTGGAGACTTCCGAGC 1288
QY 421 cctgcacagcgagcgagcgagacatgaactgtttgatgcagctccacactcttgctt 480
DB 1287 CCTGCACAGGACGCGGAGGACATGACCTGTTTATGCACTGCCACTTCTTGCTT 1228
QY 481 cctactggcgacatcctctgagcagatgagagtgctgctgtgcttcctactcctctgag 540
DB 1227 CCTACTGGGCGCACATCTGCGGCATGAGGATGCTGCGCTGCTTATCTACTCTTGGG 1168
QY 541 tctctgtgggtggcgcaatgccccttcggcgcccttcctctgcaatctcagagctcagtc 600
DB 1167 TCTTGCTGGGTGGCCAGTCCAGTCCCTGCGCTTCACTGCGCATCTCAAGGCTCAAGTC 1108
QY 601 ctggtctcgcagcatgactgggcacatgcctcactctcaagaagctcgtgtgagaca 660
DB 1107 CTGGTCTCGACGATGACCTGGGCCATGCCCTTCATCAAGAGTCTGTGTGAACCA 1048
QY 661 cgtggccagaaagtcgtgtagtgggcaagctaaaggctctcgcgcacatggtgaaact 720
DB 1047 CGTGGCCCGAGAGTTCTGATGAGGCGAGCTAAAGGGCTTCCGCCCACTGTGGAACTT 988
QY 721 ccgcaacttcagcgaccccgcaagcccaacatcttcacaaaagcccaagcgatgagcgt 780
DB 987 CCGCAACTTCAGCACACACGACCCCAACCTTCACAAAGACCCAGAGCTATACCGT 928
QY 781 ggcgcgcgttcctcctcctgggagatcagctcgtcagtagtagtgaagaagacgcagata 840
DB 927 GGGCGCGGCTTCTCTCTGGGGAGTCATCGCTCGAGTATGCAAGAAAGCAAGCAATA 868
QY 841 cctaacctaaacagcagacactgtactctctcgtatcgccgcgcgtgtcactcct 900
DB 867 CCTAACCTTCAACACGACACACCTGTACTTCTTGATCGGCGCGCGCTCTACCCCT 808
QY 901 ggtgaacttgaagtggaataatctgcgtatcagtgatgtagtgcagagtgagagatt 960
DB 807 GGTGAACCTTGAAGTGGAATAATCTGCGTACTGCTGGTGCATGCAAGTGGCGGCAATTT 748
QY 961 gctctggcgcgagcttctatgcccgtctctctactactcactccctctcagagcgt 1020
DB 747 GCTCTGGCGCGCAGCTTCTATGCGCGCTTCTTATCTACTCTCCCTTACGGCGT 688

OY	1021	ccggaggatgctgtctcttttfttgctgcgaagfcttcggaaagcaactgttctgtg	1080
OY	1021	ccggaggatgctgtctcttttfttgctgcgaagfcttcggaaagcaactgttctgtg	1080
Dd	687	CCCTGGGAGTGTCTCTCTTTTGTTGTGTGCACAGGATCTCGGAAGCACTGGATTGTGTG	628
OY	1081	gatcacacaagttagacacacalcccacaagaagatcggccacagaaacccgagactggat	1140
Dd	627	GATCACACAGATGAACACCATCCTCCCAAAGAGATCGGCCAACGAAAGCACCCGGACTGGGT	568
OY	1141	cagctcttaagcttgcagaccacatgcgtgaagaccttaacttltoaccaacttgttcaag	1200
Dd	567	CAGCTCTAAGTGTGGACACCACCTGCACAACGGGAGCCCTCACTTTTCACCAACTGGTTGAG	508
OY	1201	cggagaccctaacttcacagatcgagacacacccctctccccagatattgcagagacaacta	1260
Dd	507	CGGGACACTCAACTTCCAAGATCAGACACCACTCTTCCCCAGAGATCCGAGACACACTTA	448
OY	1261	cagccgagttgcccgcgcttgcagatgcgtgtgtgtgcgaagcagcagcctcagatacgaagt	1320
Dd	447	CAGCGCGGTGGCCCCCGCTGGTCAAGTGTGCTGTGTGCAGACACGGGCTCAGCTACGANGT	388
OY	1321	gaagcccttcctcaacgcgcgtgtgtgtgacatcgttcagttccctgaagaagtttgtgtgaat	1380
Dd	387	GAAGCCCTTCCTCTCAACGCGCTGTGTGAACATGTCAGAGTCTCTGAAGAAGTCTGTGACAT	328
OY	1381	ctggctggaagcgtctactccatcatcagtagtgaagacacacccagcggcgagagaaggtcca	1440
Dd	327	CTGGCTGGAGCGCTCACTCCATCATCAGTAGAAGGCAACCCAGCGGGGAGAAAGSGCTCA	268
OY	1441	gggacacagcaaaccaagcgaagcccccgaggagatcgatacccccaacctcaactgacca	1500
Dd	267	GGGACACGACCAACCAACCCAGCCCCGGCGGGATGCATATCCCACCCCTCCACATGGGCA	208
OY	1501	gccctggaggatgcactgcctccctcctgtgtactgtgtcttccctcgcgccccctcaat	1560
Dd	207	GCTTGGGGTGTCCCTGCTGCTGCTCCTCTGTGTGTGTGTCTTCCCTCGGCCCTCACAT	148
OY	1561	gtgtattccagcagccctaatgacctgtgcttgccttgcctgagctgtagacagggtagaaggag	1620
Dd	147	GGTATTTCAGAGAGCCCATATGTGCTTGGCTTGGGCTGATGGGACAGGGGTAGAGGGAG	88
OY	1621	gtgagcatagacacatttccatagcgaagaattgggggaagctgttattttataattaa	1680
Dd	87	GTCAGCATAGACACTTTTCTTAGAGCGAGATAATGGGGGAAAAGCTGTATTATTTATATTA	28
OY	1681	aatacatlcagaatgtaaaaa 1700	
Dd	27	AATACATTCAAGATGTAAAAA 8	
<hr/>			
RESULT 3			
ID	AAA90954	standard; cDNA; 1757 BP.	
XX	AAA90954;		
AC	15-JAN-2001	(first entry)	
DE	Human fatty acid desaturase 3 coding sequence.		
KM	Human; fatty acid desaturase; FADS-1; FADS-2; FADS-3; gene therapy;		
OS	Liver disease; coronary artery disease; cancer; ss.		
XX	Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	CDS	134..1471	
FT	/tag= a		
FT	/product= FADS-3		
XX	EP1035207-A1.		
PN			
DD	13-SEP-2000.		
XX			

PF 09-MAR-1999; 99EP-0104664.
 PR 09-MAR-1999; 99EP-0104664.
 XX
 PA (MULT-) MULTIGENE BIOTECH GMBH.
 XX
 PI Weber BHF, Marguardt A;
 XX
 DR WPI; 2000-559875/52.
 XX P-PSDB; AAY97540.
 PT
 PT Novel cDNA molecules encoding three human fatty acid desaturases,
 PS FADS1, FADS2 and FADS3, useful in the treatment of liver disease,
 PS coronary artery disease and cancer -
 PS
 PS Claim 2; Page 38-39; 72pp; English.
 CC This sequence encodes the human fatty acid desaturase, FADS-3, of the
 CC invention. An antibody directed against the 3 FADS molecule of the
 CC invention (FADS-1, FADS-2, and FADS-3) is useful for diagnostic or
 CC therapeutic purposes. The FADS coding sequences are useful in gene
 CC therapy. The polypeptide and antibodies are useful in screening for
 CC modulating drugs. The polypeptides are also useful for treating liver
 CC disease, coronary artery disease and cancer.
 CC Note: Two copies of the sequence listing are present within this
 CC patent, which contain different sequences. AAA90952 and AAA90955 are
 CC both stated as being SEQ ID 1. AAA90956-A90971, and AAA90972-A90987 are
 CC stated as being SEQ ID's 7-22.
 XX
 SEQ Sequence 1757 BP; 318 A; 580 C; 517 G; 342 T; 0 other;

Query Match	98.9%	Score 1681.4	DB 21	Length 1757	
Best Local Similarity	99.9%	Pred. No. 0			
Matches 1693	Conservative	0	Matches	1	Indels 1
					Gaps 1
QY	1	cttcgcttcctccgcagagcttgcttgctcgagacctcgacacgcgcctcggtgaccccaagatcgc	60		
Db	64	cttcgcttcctccgcagagcttgcttgctcgagacctcgacacgcgcctcggtgaccccaagatcgc	123		
QY	61	tgcgtgcagcatggcggcgcttcggggagccggagccgcggggagggagccgcgcagccggg	120		
Db	124	tgcgtgcagcatggcggcgcttcggggagccggagccgcggggagggagccgcgcagccggg	183		
QY	121	ggcacccgttcggcccaactcttgcttggtggagacagatccgcgcgcacgcacccgcgcggagaaa	180		
Db	184	ggcacccgttcggcccaactcttcggtggagacagatccgcgcgcacgcacccgcgcggagaaa	243		
QY	181	gtggtctgttcacgcagccgcgcgttcctaaagaaatcacgcgcgttcgggagacagcgacacccgg	240		
Db	244	gtggtctgttcacgcagccgcgcgttcctaaagaaatcacgcgcgttcgggagacagcgacacccgg	303		
QY	241	gggcagccgcctcatcgcgcacacacgcgcgttcgagagacgcacaggaatgccttcgcgttc	300		
Db	304	gggcagccgcctcatcgcgcacacacgcgcgttcgagagacgcacaggaatgccttcgcgttc	363		
QY	301	ccatcaaatcatccaatttctgtgcgcgaagtcttcctacagcccttggtgatctggagagctggc	360		
Db	364	ccatcaaatcatccaatttctgtgcgcgaagtcttcctacagcccttggtgatctggagagctggc	423		
QY	361	tccggaagaaacccagccagcagatggagaccccttaatatgcgcagcttggttcgagagcttcgcagc	420		
Db	424	tccggaagaaacccagccagcagatggagaccccttaatatgcgcagcttggttcgagagcttcgcagc	483		
QY	421	ccctgcacacagccagccgcagagacatggaagcttggttggatggcagtcacatccacctcttgctt	480		
Db	484	ccctgcacacagccagccgcagagacatggaagcttggttggatggcagtcacatccacctcttgctt	543		
QY	481	ccctactgggcacacatccctgcgcgcacatggagagtgctctggccttggtctcttatccacccctggg	540		
Db	544	ccctactgggcacacatccctgcgcgcacatggagagtgctctggccttggtctcttatccacccctggg	603		
QY	541	tctctgctgtggttcgcaggtgccttcggcgcgccttcacatccctgcgcacatctctacagcttcacgc	600		

```
Db      604 tctctgctgggtgcccagtcgccccttcacaccccttcgacatcttcacagctcagtc 663
Qy      601 ctgtgtctgcagcatgacctgggcatgctccatcttcacagaaagctctgttgaaaca 660
Db      664 ctgtgtctgcagcatgacctgggcatgctccatcttcacagaaagctctgttgaaaca 723
Qy      661 cgtgcccagaaagctcgtgtagtgggagctaaaggctctccgcacatggtgaaact 720
Db      724 cgtgcccagaaagctcgtgtagtgggagctaaaggctctccgcacatggtgaaact 783
Qy      721 ccgcacattccagcaacacgcccagcccaacatcttcacaaagacccagaaagctgagct 780
Db      784 ccgcacattccagcaacacgcccagcccaacatcttcacaaagacccagaaagctgagct 843
Qy      781 ggcgcgcgtcttcctctctgtagtggagtcacgctcgtgtagtggcaagaagaaacgagata 840
Db      844 ggcgcgcgtcttcctctctgtagtggagtcacgctcgtgtagtggcaagaagaaacgagata 903
Qy      841 cctacacctacaacagcaagcaacactgactctctctgtagtggccgcgctgctacacct 900
Db      904 cctacacctacaacagcaagcaacactgactctctctgtagtggccgcgctgctacacct 963
Qy      901 ggtgaaacttgtagtggaaatctggcgtacatgctggtgtagtggagtgagtgagtgatt 960
Db      964 ggtgaaacttgtagtggaaatctggcgtacatgctggtgtagtggagtgagtgagtgatt 1023
Qy      961 ggcctggccgcagctctctctctctctctctctctctctctctctctctctctctctct 1020
Db      1024 gctctggccgcagctctctctctctctctctctctctctctctctctctctctctctct 1083
Qy      1021 cctctggggtgctgctctctctctctctctctctctctctctctctctctctctctct 1080
Db      1084 cctctggggtgctgctctctctctctctctctctctctctctctctctctctctctct 1143
Qy      1081 gatcacacagatgaacacacaccccaagagatcggcagcagaaagacccggagacgtggt 1140
Db      1144 gatcacacagatgaacacacaccccaagagatcggcagcagaaagacccggagacgtggt 1203
Qy      1141 cagctctcagctgtagcagcagcctgtagcagctgtagcagcctctctctctctctctct 1200
Db      1204 cagctctcagctgtagcagcagcctgtagcagctgtagcagcctctctctctctctct 1263
Qy      1201 cgggacactcaactctcagatcagacacacacacacacacacacacacacacacacac 1260
Db      1264 cgggacactcaactctcagatcagacacacacacacacacacacacacacacacacac 1323
Qy      1261 cagcggggtgtagcggcgtgtagcagctgtagcagctgtagcagcctcagctcagctgag 1320
Db      1324 cagcggggtgtagcggcgtgtagcagctgtagcagctgtagcagcctcagctcagctgag 1383
Qy      1321 gaagccctctcagcagcagctgtagcagctgtagcagctgtagcagctgtagcagctgtag 1380
Db      1384 gaagccctctcagcagcagctgtagcagctgtagcagctgtagcagctgtagcagctgtag 1443
Qy      1381 ctgtgctgtagcagctcagctcagatgtagaagcaacacacacacacacacacacacacac 1440
Db      1444 ctgtgctgtagcagctcagctcagatgtagaagcaacacacacacacacacacacacacac 1503
Qy      1441 gggagcagcaacaaagcagcccgccgggagatgtagaataccccacacacacacacacacac 1500
Db      1504 gggagcagcaacaaagcagcccgccgggagatgtagaataccccacacacacacacacacac 1562
Qy      1501 ggcctggggtgtagcagctgctcctcctcgtgtagctgtgtctctccctcgcgcctcagat 1560
Db      1563 ggcctggggtgtagcagctgctcctcctcgtgtagctgtgtgtctccctcgcgcctcagat 1622
Qy      1561 gctgattcagagcagcctatgctgctgctgctgctgctgctgctgctgctgctgctgctg 1620
Db      1623 gctgattcagagcagcctatgctgctgctgctgctgctgctgctgctgctgctgctgctg 1682
Qy      1621 gtagagcagacattctcctcagagcagagatgtaggagaaagctgattattatataa 1680
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Db      1683 gtagagcagacacattctcctcagagcagagattgtaggagaaagcgttattattataa 1742
Qy      1681 aatacatcagatgt 1695
Db      1743 aatacatcagatgt 1757

RESULT 4
AA574468
ID   AA574468 standard; cDNA; 1663 BP.
XX
AC   AA574468;
XX
DT   13-FEB-2002 (first entry)
XX
DE   DNA encoding novel human diagnostic protein #10272.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
XX   23-AUG-2000; 2000US-0649167.
XX
PA   (HSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
DR   WPI: 2001-639362/73.
DR   P-PSDB: ABG10281.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
XX   diagnostics, forensics, gene mapping, identification of mutations
XX   responsible for genetic disorders or other traits and to assess
XX   biodiversity -
XX
PS   Claim 1; SEQ ID No 10272; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
XX   polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX   and gene mapping, and in recombinant production of (II). The
XX   polynucleotides are also used in diagnostics as expressed sequence tags
XX   for identifying expressed genes. (I) is useful in gene therapy techniques
XX   to restore normal activity of (II) or to treat disease states involving
XX   (II). (II) is useful for generating antibodies against it, detecting or
XX   quantitating a polypeptide in tissue, as molecular weight markers and as
XX   a food supplement. (II) and its binding partners are useful in medical
XX   imaging of sites expressing (II). (I) and (II) are useful for treating
XX   disorders involving aberrant protein expression or biological activity.
XX   The polypeptide and polynucleotide sequences have applications in
XX   diagnostics, forensics, gene mapping, identification of mutations
XX   responsible for genetic disorders or other traits to assess biodiversity
XX   and to produce other types of data and products dependent on DNA and
XX   amino acid sequences. AA564197-AA594564 represent novel human
XX   diagnostic coding sequences of the invention.
XX   Note: The sequence data for this patent did not appear in the printed
XX   specification, but was obtained in electronic format directly from WIPO
XX   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1663 BP; 332 A; 538 G; 458 C; 335 T; 0 other;
```

Query Match 84.9%; Score 1443.8; DB 23; Length 1663;
Best Local Similarity 97.8%; Pred. No: 6.1e-313;
Matches 1613; Conservative 0; Mismatches 17; Indels 19; Gaps 14;

[illegible]

QY	1143	gctctacgctgagagcaccactgtgaaagtggagccctaac-ttttaccaaactgtgttcagc	1201
Db	1081	gctctacgctgagagcaccactgtgaaagtggagccctaacgttttccaccaaactgtgttcagc	1140
QY	1202	ggcaccctcaacttccagatctgagaccaccactttcccccagagatgcccagagacaa-cia	1260
Db	1141	ggcaccctcaacttccagatctgagaccaccactttcccccagagatgcccagagacaaacta	1200
QY	1261	cagccgggtgtgcccgcgc-tgttcaagtctgctgtgtgcc-aagcagggcctcaagtacg-a	1317
Db	1201	cagccgggtgtgcccgcgcctgtgttcaagctgctgtgtgtccaaagcagggcctcaagtacgaa	1260
QY	1318	agtgaagcccttc-caccccgctgtgtgtgacatctgtccagatgtccctgaag-aagtgtgt	1375
Db	1261	agtgaagcccttccttcttccaccgcgcgtgtgtgtgacatctgtccagatgtccctgaagatctgtgt	1320
QY	1376	gacatctgtgctgagcagctacctccatcagtgtaaggaacaacaccagcgggcagagaaag	1435
Db	1321	gacatctgtgctgagcagctacctccatcagtgtaaggaacaacaccagcgggcagagaaag	1380
QY	1436	gtctcaaggagaccaggaaccgaagcc-agcccccggtggatctga--taaccccaacccctcc	1492
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DT	28-JAN-1999	(first entry)	
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KM	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;		
KM	developmental abnormality; foetal deficiency; blood; allergy; renal; ds;		
KM	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;		
KM	inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;		
KM	cognitive disorder; schizophrenia; prostate; osteitis; osteoclast; thymus;		
KM	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;		
KM	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.		
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OS	Homo sapiens.		
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PR	07-MAR-1997;	97US-0040162.	
PR	07-MAR-1997;	97US-0040163.	
PR	07-MAR-1997;	97US-0040333.	

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KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukemia;		
KW	developmental abnormality; foetal deficiency; blood; allergy; renal; ds;		
KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;		
KW	inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;		
KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;		
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KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.		
XX			
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PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057761.
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PA (HUMA-) HUMAN GENOME SCI INC.
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PI Bednarik DP, Brewer LA, Carter KC, Duan R, Edner R, Endress GA,
PI Feng P, Ferlie AM, Fischer CL, Graves KA, Greene JM, Hu JS,
PI Kyaw H, Laflair DW, Li Y, Moore PA, Ni J, Olsen RS, Rosen CA,
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX WPI; 1998-60987/51.
XX P-PSDB; AAW75165.
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PT New isolated human genes and the secreted polypeptides they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PS disorders, immune diseases, inflammation or blood disorders
PS
XX Claim 1: Page 262-264; 447pp; English.
XX
CC This sequence represents a nucleic acid molecule which encodes a
CC secreted human protein. The gene number, and the clone it is derived
CC from, are detailed in the descriptor line. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV34145) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 70 novel genes and their fragments (nucleic
CC acid sequences: AAV34154-V34276; amino acid sequences AAW75057-W75179)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 70
CC polynucleotides, based on which tissues they are most highly expressed in
XX (see AAV34154 for described uses).
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SQ Sequence 2016 BP; 401 A; 629 C; 563 G; 412 T; 11 other.

Query Match 54.48; Score 924.2; DB 19; Length 2016;
Best Local Similarity 77.08; Pred. No. 7.1e-197;
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2002, 01:41:20 ; Search time 4866.45 Seconds
(without alignments)
4714.900 Million cell updates/sec

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Searched: 13736207 seqs, 6748477542 residues 27472414

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
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5	773.4	45.5	849	10	BI254370 602976675
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SOURCE human.
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REFERENCE 1 (bases 1 to 962)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.

FEATURES

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/dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
/lab_host="DH10B"
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestechn.com URL : http://fulllength.invitrogen.com"
BASE COUNT 166 a 325 c 290 g 178 t 3 others

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Db 600 caccactgttccagcggccacactcagatcgagatcgagcaccacttccaggat 659
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QY 1246 gcgagacacacacacagcgggtgccccgtgtcaagctgtgtgccaagacgg 1305
|||||
Db 660 gcgagacacacacacagcgggtgccccgtgtcaagctgtgtgccaagacgg 719
|||||
QY 1306 cctcagctcagagtgaaaccccttctcctcagcgtgtgtgagatcgtcagcttga 1365
|||||
Db 720 gctcagctcagagtgaaaccccttctcctcagcgtgtgtgagatcgtcagcttga 779
|||||
QY 1366 gaagctgtgacatctgtcgtgagcgtcactcactcagtgaaaggcaaccagcg 1425
|||||
Db 780 gaagctgtgacatctgtcgtgagcgtcactcactcagtgaaaggcaaccagcg 839
|||||
QY 1426 gcagagaagggtcgaaggcaaccga 1451
|||||
Db 840 gcagagaagggtcgaaggcaaccga 865
|||||

RESULT 3
BI821778 883 bp mRNA linear EST 04-OCT-2001
LOCUS BI821778 603035847F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5176906 5',
DEFINITION mRNA sequence.
ACCESSION BI821778
VERSION BI821778.1 GI:15933328
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 883)
NIH-MGC http://mgi.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-femail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11440 row: n column: 11
High quality sequence stop: 783.
Location/Qualifiers
1. 883
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5176906"
/clone_1id="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH-MGC Library."

BASE COUNT 165 a 285 c 262 g 171 t
ORIGIN

Query Match 46.1%; Score 783.2; DB 10; Length 883;
Best Local Similarity 95.7%; Pred. No. 3,4e-154;

Matches 848; Conservative 0; Mismatches 33; Indels 5; Gaps 4;

QY 70 catgycgycgtcgggagccggagccgcyggagagccgcgcagccggggccgcct 129
|||||
Db 1 CATGGGCGCGCTCGGGGAGCGGGACCGCGGAGGAGACCGCGAGCGGGGACCGCT 60
|||||
QY 130 gccacacttctgtcgtgggagcagatccggggcagaccagccggcgagacagtgtgt 189
|||||
Db 61 gccacacttctgtcgtgggagcagatccggggcagaccagccggcgagacagtgtgt 120
|||||
QY 190 catcagcgcgcgctctacacatcagcgcgtgtggcacaagcggcaccagggggcagcg 249
|||||
Db 121 catcagcgcgcgcgtctacacatcagcgcgtgtggcacaagcggcaccagggggcagcg 179
|||||
QY 250 cctcactcggccaaccaagcgcgtgtgagagcgcagagatgcttccgttccatcaaga 309
|||||
Db 180 cctcactcggccaaccaagcgcgtgtgagagcgcagagatgcttccgttccatcaaga 239
|||||
QY 310 tctcaatttctgtcgaagttctcagccctctgtgtgtgtgagatcgtctccggaaga 369
|||||
Db 240 tctcaatttctgtcgaagttctcagccctctgtgtgtgtgagatcgtctccggaaga 299
|||||
QY 370 acccagcagagatgaccccttgaatgcagctgtgtcgaagacttcgaaccctcgacca 429
|||||
Db 300 acccagcagagatgaccccttgaatgcagctgtgtcgaagacttcgaaccctcgacca 359
|||||
QY 430 ggcagcgcagagacatgaagctgtgtgagcagctcctccttctgttccactaggg 489
|||||
Db 360 ggcagcgcagagacatgaagctgtgtgagcagctcctccttctgttccactaggg 419
|||||
QY 490 ccaatctctgcacatgagatgtgtcgtcgtcttacttactcctcctgtgtctgtgtg 549
|||||
Db 420 ccaatctctgcacatgagatgtgtcgtcgtcttacttactcctcctgtgtgtgtg 479
|||||
QY 550 ggtgcagctgcctcgtgcgcctcactcctcagctcctcagctcagctgtgtct 609
|||||
Db 480 ggtgcagctgcctcgtgcgcctcactcctcagctcctcagctcagctgtgtct 539
|||||
QY 610 gcaagctgcctcgtgcgcctcactcctcagctcctcagctcctcagctgtgtct 669
|||||
Db 540 gcaagctgcctcgtgcgcctcactcctcagctcctcagctcctcagctgtgtct 599
|||||
QY 670 gaagctcgtatgagcgaactaaggctctcgcgcctcctcgtgtgaattccgcaact 729
|||||
Db 600 gaagctcgtatgagcgaactaaggctctcgcgcctcctcgtgtgaattccgcaact 659
|||||
QY 730 ccagcaccagcgaagcccaaatcttccacaagaaccagcgcgtgtgtgtgtgtgt 789
|||||
Db 660 ccagcaccagcgaagcccaaatcttccacaagaaccagcgcgtgtgtgtgtgtgt 718
|||||
QY 790 ctcccccctggggg--gtcatcgtcgtatgtatgcaagaagaacagcagatactacc 847
|||||
Db 719 ctcccccctggggg--gtcatcgtcgtatgtatgcaagaagaacagcagatactacc 778
|||||
QY 848 tacaacacagcagacctgtactcttccctgtatgtgcgcgcgcgtctcaccctgtgtaac 907
|||||
Db 779 AAAACAGAAACACCTTAACCTTCTTCATGATGGGCGCGGCTGTTCACCTGGTGAGC 838
|||||
QY 908 tttagaagtgaataatcgtgtgtatcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 953
|||||
Db 839 tttagaagtgtg-AAATTTGGCGTATATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 883
|||||

RESULT 4
BG753978 832 bp mRNA linear EST 15-MAY-2001
LOCUS 602709505F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846153 5',
DEFINITION mRNA sequence.
ACCESSION BG753978
VERSION BG753978.1 GI:14064631
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 832)
NIH_MGC http://mgc.ncl.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLCM1686 row: 1 column: 02
High quality sequence stop: 831.
Location/Qualifiers
1. 832
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4846153"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming;
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 164 a 284 c 217 g 167 t
ORIGIN
Query Match 45.8%; Score 778.4; DB 10; Length 832;
Best Local Similarity 98.2%; Pred. No. 3.4e-153;
Matches 819; Conservative 0; Mismatches 11; Indels 4; Gaps 3;
QY 721 ccgcacttcagacacagcccaacatctccacaagaagccagagtgagct 780
Db 2 CCGGCACCTTCAGACACACCCCAAGCCCAACATCTCCAAAGAGCCAGACGTGACGGT 61
QY 781 gggccgcgtctctctctggggagatcacgcgcagatgagcaagaagaagagagata 840
Db 62 GGGCCCGGCTCTCTCTGGGGAGGTATCCGTCGAGATGCGAAGAGAGACGCGAGATA 121
QY 841 cctacacctacaacagagacagctgtactctctctgacagccgcgcgctgtcacct 900
Db 122 CCTACCTTACAAACAGACAGCAGCTGTACTTCTTCGATGCGCCCGCTGCTCACCT 181
QY 901 ggtgaacttggaaatggaatctggcgatcatagctgggtgtgataagtgagcgatt 960
Db 182 GGTGAACCTTGAATGGAATCTGGCGTACATGCGGTGTCATCAGTGGGCGGATT 241
QY 961 gctctgggcccagctctctatgcccgcctctctctatccctaccccttaagcgct 1020
Db 242 GCTCTGGGCCCGCAGCTTCTATGCCCGCTCTCTTACTTACCTCCCTTCTACGGCGT 301

QY 1021 ccctggggtgctgctctctcttctgtgtcaggtgcttgaaagccactggtgtg 1080
Db 302 CCTGGGGGTCTCTCTCTTGTGTCTGTCAAGGGCTCGGAACCCACTGGTGTG 361
QY 1081 gatcacagatgaacacatccccaagagatcggccacgagacccggagctgggt 1140
Db 362 GATCACAGATGAACACATCCCCAAAGAGATGGGCCAGAGAACGCCGGAATGGGT 421
QY 1141 caagctcaagctggcagccaactgtaacgltgagccctactttcaccaactgttaag 1200
Db 422 CAGCTTCACCTGGACGCCACCTGCAACGTGAGCCCTTCACTTTCACCAACTGGTTGAG 481
QY 1201 cgggacacttaactccaagatcgagcaccaacctctccccaagatgcgagacaacta 1260
Db 482 CGGGACCTTAACCTTCCAAATGAGCAGCAGCTTCCCGAGATGCGAGACACACTA 541
QY 1261 caagcgggtggcccgctgtgtaagctgctgtgtgccaagacggcctcaagctgaagt 1320
Db 542 CAGCGGGGGGGCCCGCTGCTCAAGTCTGTCGTCAGCAGCGCTCAGCTTACGAAGT 601
QY 1321 gaagccctctcaacggcggtgtgagacatgctcaagctcccgaaagaagctggtgacat 1380
Db 602 GAAGCCCTTCTCAACGCGCTGTGTGACATCGTCAAGTCTGAAAGATCTGTGACAT 661
QY 1381 ctggtgtgacgcttacatccatcatcagtgaaagacacacccagcgaggcagagaaggtctca 1440
Db 662 CTGGCTGAGCGCTTACCTTCATCATGTAAGGCACACCCAGCGGGGAGAGAGGGCTCA 721
QY 1441 gggacacgaacaaagcagcccgcggtgagatgataccccaccctccatcagggca 1500
Db 722 GGGACACGACAAACAAAGCCAG-CCCGGGGGGATGCAT-CCCAACCCCTTCAGTGTCA 779
QY 1501 gctctgggtgctgctgctccctctgtgactgtgtgtcttccctcgcgcccc 1554
Db 780 GCTCTGGGGGTCTTGTCTTGTCC--CTGATGACTGTGTCTTCTCCGTCGCGCCCTC 831
RESULT 5
BI254370 849 bp mRNA linear EST 17-JUL-2001
LOCUS 60297675F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5115666 5',
DEFINITION mRNA sequence.
ACCESSION BI254370
VERSION BI254370.1 GI:14806710
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 849)
NIH_MGC http://mgc.ncl.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLCM1281 row: f column: 19
High quality sequence stop: 847.
Location/Qualifiers
1. 849
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5115666"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-Sport0; Site_1: NotI;

Db 362 GATCACAAGATGACACATCCCAAGAGATTCGGCCACGAAAGACCCGGAGCTGGGT 421

Qy 1141 cagctctcagctgagcagccaccctgcaagctgagccctcatttccaccaattggtcag 1200
|||||
Db 422 CAGCTCTCAGCTGGGAGGACCTGGACAGCTGGAGCCCTACTTTCACCAACTGGTTTCA 481
|||||

Qy 1201 cgggcaactcaactccagatcgagacacacacttccccagatgacgagacacacta 1260
|||||
Db 482 CCGGCAACCTCAACTCCAGATGAGACACACCTCTTCCCAAGATGCGAGACACACTA 541
|||||

Qy 1261 cagccgggtgagcccgctgagtcagctgctgctgctcagaagcagccgctcagtaagaat 1320
|||||
Db 542 CAGCCGGGAGGCCCCCGCTGGTCAAGTGGCTGTGTGCCAAGCAGCGCTCAGCTACGAAGT 601
|||||

Qy 1321 gaagccctctcctcaccgagctggtgagacatcgtlccctgtaagaagctggtgacat 1380
|||||
Db 602 GAAGCCCTTCTCTCACCAGCGCTGGTGGACATGCTCAGTCCCTGAAGAAGTGTGTGACAT 661
|||||

Qy 1381 ctgagctgagagcctaccctccatcagtgaaagaaacacccagggcagagagaaggtctca 1440
|||||
Db 662 CTGGCTGGAGCGCTACCTTCATCACTGAAGGACACCCAGCGGGCAGAGAGGGCTCA 721
|||||

Qy 1441 gggcaccagcaacccaagcagcccgagcgagatcgatataccccccctcactgagcca 1500
|||||
Db 722 GGGCACAAGCAACCAAGCAGCGCCCGGGGATTCGATACCCCAACTCTCAGTGGCCA 781
|||||

Qy 1501 gcttgagggtgctc 1512
|||||
Db 782 GCTGGGGGTGGC 793
|||||

RESULT 7
LOCUS AL537073 833 bp mRNA linear EST 13-FEB-2001
DEFINITION AL537073 LTI_FLO13_FBrnl Homo sapiens cDNA clone CS0DF019YB01 3
prime, mRNA sequence.
ACCESSION AL537073
VERSION AL537073.1 GI:12800566
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 833)
AUTHORS Li, M.B., Gruber, C., Jeesee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Source
1..833
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DF019YB01"
/clone_1b="LTI_FLO13_FBrnl"
/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
/lab_host="DH10B"
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 171 a 213 c 277 g 150 t 22 others

Query Match 43.7%; Score 742.8; DB 9; Length 833;
Best Local Similarity 93.0%; Pred. No. 1e-145;
Matches 775; Conservative 19; Mismatches 12; Indels 27; Gaps 1;

Qy 826 gaagaaacgcagatacctacctaacaacagcagcactgtacttctctcgtatcgccc 885
|||||
Db 833 GAAGAAAGCGAGATACCTACCCCTCAACCAAGCAGACCTTACTCTTCTGATCGGCC 774
|||||

Qy 886 ggcgcgtcacccttggtgaacttgaagtggaaatctggcgtlaactgctggtgcat 945
|||||
Db 773 SCGCTCTCACCCTGGTGAACCTTGAAGTGAAGAAATCTGGCTACATGCTGTGTCAT 714
|||||

Qy 946 gcaatggagcagattgtctcggcgccagctctatgcccgtctctctacact 1005
|||||
Db 713 GCAATGGGCGGATTTGCTCTGGGCGCCAGCTTCTATGCCGCTTCTTATCTACCT 654
|||||

Qy 1006 ccccttaagcgctccctgggtgctgctctctcttcttctgctgcaaggtcctggaag 1065
|||||
Db 653 CCCCTTCTACGGCGCTCCCTGGGGTGTGCTCTTGTGTGCTGTGAGGCTCTGGAAG 594
|||||

Qy 1066 ccaatggtctggtgagtaacagatgaacacacatccccaaagaaatcgccagagaa 1125
|||||
Db 593 CCACTGTTGCTGTGATCAACAGATGAACACATCCCAAGAGATGGCCACGAGAA 534
|||||

Qy 1126 gcaacggagactgggtcagctctcagctgagccacctgaaagctgagccctcacttt 1185
|||||
Db 533 GCACCGGAGCTGGGTCAGCTCTCAGTGGGAGCCAGCTGGAAGTGGAGCCCTCATTTT 474
|||||

Qy 1186 gaccaactggttaagcgggagcactcaactcagatcgagcaca----- 1230
|||||
Db 473 CACCAACTGTTTACGGGGAGGAGCTCAACTTCCAGATCGAGCACAGTGCAGATACGNT 414
|||||

Qy 1231 -----cctctcccaagatgcccagagacaactcagccggttgcccgct 1278
|||||
Db 413 CCCCAACCCCAAGCTTTTCCCGAGATGCCGAGACACAACTACAGCGGGGCGCCGCT 354
|||||

Qy 1279 gttcaagctgctgtgtgccaagcagcctcagctcagatgaagtgaaagccctcctcagcc 1338
|||||
Db 353 GGTCAAGTCTCTTTTGGCCAAAGCAGCGCTCAGCTACGATGGAAGGAAACCTTCTCAGCGC 294
|||||

Qy 1339 gctggtgagatgctgaaggtccctcctgaagaagctggtgacatcctgctgagcgtact 1398
|||||
Db 293 GCTGTGTGAGATGTGATGATGCTCTGAAGAGTGTGTGACATCTGGCTGGAGCGCTACT 234
|||||

Qy 1399 ccatactgaagcaacacacccaagcgagagaaaggtcagagcagcagaacaaacagc 1458
|||||
Db 233 CCAATGATGAAGCAACACCCAGCGCGGCGRGAAGAGGATCAGGCRCCMCAACCAACC 174
|||||

Qy 1459 cagcccccggggagatcgatacccccccctcactgagcagcctggtggtgctgctcc 1518
|||||
Db 173 CMCSCCCSCGSGSMTCMTACCCCAACCCCTCMCTGCGCMSCGSGGGGSGSCCYGCG 114
|||||

Qy 1519 tgcctcctgtagctgttctctccctggccctcagctcagtgattatcagacacctta 1578
|||||
Db 113 TGCCCCCCTGTGATCTTTGCTTTTCTGTGCCCTCTCATGTGTATTCACACCCCTTA 54
|||||

Qy 1579 tggccttgactcggcctgatatgagcagaggttagaggaaggttagcctagc 1631
|||||
Db 53 TGCGCTTGCGCTCGGCTTGATGGAGCAGGGGTAGAGGGAAGTGAAGCATNCC 1
|||||

RESULT 8
LOCUS BG747608 738 bp mRNA linear EST 15-MAY-2001
DEFINITION 602705067F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4841848 5',
mRNA sequence.
ACCESSION BG747608
VERSION BG747608.1 GI:14058261
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

QY 721 ccgcacactccagcaccagcccaaatcttccacaagaagccagacgtacgt 780
DB 738 CCG-CACCTTCAGCACCAGCCAGCAACATCTTCACAAAGACCAGAGTACGGT 796
QY 781 ggcgc 786
DB 797 GCGGCC 802

RESULT 11
BG755586 840 bp mRNA linear EST 15-MAY-2001
LOCUS 602716270F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4856584 5',
mRNA sequence.
ACCESSION BG755586
VERSION BG755586.1 GI:14066239
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mhc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cga@bbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LNCM1707 row: k column: 17
High quality sequence stop: 825.

FEATURES
source
1. 840
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4856584"
/clone_lib="NIH_MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAGG. Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald W. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC library."

BASE COUNT
150 a 263 c 226 g 201 t

ORIGIN
Query Match 39.9%; Score 678; DB 10; Length 840;
Best Local Similarity 98.7%; Pred. No. 4,1e-132;
Matches 736; Conservative 0; Mismatches 5; Indels 5; Gaps 5;

QY 283 ggaatcctcgtgctccatcaaatcttggcgaagttctcagccct 342
DB 85 GGAATGCTTCGCTTCATCAATGATCTCAATTTGGCGCAAGTCTACAGCCCT 144
QY 343 gttgatggaagctggcgcgaagaaccagcagatgacccctgaatgcagct 402
DB 145 GTTGATTTGAGAGCTGGCTCCGAAAGACCCAGAGGAGCCCTTAATGCGAGCT 204
QY 403 ggtcagagactccagacccctgaccagcagccgagagacatgaatgtttgatccag 462
DB 205 GGTGAGAGACTTCGAGCCCTGCACAGGACGCCGAGGAGCAATGACTTTTGATGCCAG 264

QY 463 tcccaactctcttgcttccactactggtggcacaatccctggtccatggaagtgtcgtgct 522
DB 265 TCCACACTCTTTGCTTCCATCTGAGGCGACATCTGGCCATGAGAGTGTGCTGGCTGGCT 324
QY 523 ccttatactcctcgtggtcgtggtggtcgcagtgccctggtgcagcttccatcctggtgc 582
DB 325 CCTATCTACCTCTGGGTCTGGGTGGGTGGGTCCAGTGCCTGGCCGCCCTTTCATCTGGC 384
QY 583 catctcaggtcagtcagtcgtgtctgcaagcagtcagtcagtcagtcagtcagtcagtc 642
DB 385 CATCTCTCAGGCTCAGTCTGCTGCTGCTCAGCAGTACAGTACAGTACAGTACAGTACAG 444
QY 643 gaatgctcgtgtggaacacagtcgtgcccagaagttcgtatggtggcagctaaaggctctc 702
DB 445 GAAGTCTGTGTGGAACCACTGAGCCCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 504
QY 703 cgcacactggtggaactcgcgcacactccacacacacacacacacacacacacacacac 762
DB 505 CGCCACTGTGTGAGACTTCCGCCACTTCACAGCACACACACACACACACACACATCTTCA 564
QY 763 agaccacagctgacggtggtggtcgtctcctcctggtggtggtggtggtggtggtggt 822
DB 565 AGACCCAGACGTGAGCGTGGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 624
QY 823 caagaagaagcagacatacctaccctacacacacacacacacacacacacacacacacac 882
DB 625 CAAAGAAAGACGAGATACCTACCTACACACACACACACACACACACCTGTCTCTCTCT 684
QY 883 cccgcgcg-cgtcacctcgtgtaactggaagtggaaatcgtggtacatggtgtgt 941
DB 685 CCGCGCGCTTGTCTACCTCTGTGTGAACTTGAAGTGGAAATCTGGCTACATGCTGTGT 744
QY 942 gcatcagctggcggatctgctcgtggtggtggtggtggtggtggtggtggtggtggt 1001
DB 745 GCATCAGTGGGCGGA-TTGCCTGGGCGG-CAGGCTGTATGCGG-TTCTTCTATACCG 801
QY 1002 acctccctctcaggggtccctggg 1027
DB 802 TACT-CCCTTCTACGCGCTCTGGGG 826

RESULT 12
BG826581 1107 bp mRNA linear EST 22-MAY-2001
LOCUS 60275027F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4902835 5',
mRNA sequence.
ACCESSION BG826581
VERSION BG826581.1 GI:14174168
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mhc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LNCM1800 row: b column: 20
High quality sequence stop: 778.

FEATURES
source
1. 1107
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4902835"

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/clone_lib="NIH_MGC_17"
/tissue_type="rhinobdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: muscle; Vector: pORF7; Site:1: EcoRI;
Site:2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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BASE COUNT      208 a      349 c      348 g      202 t
ORIGIN
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Query Match      39.2%; Score 666.4; DB 10; Length 1107;
Best Local Similarity 87.7%; Pred. No. 1.2e-129;
Matches 849; Conservative 0; Mismatches 91; Indels 28; Gaps 10;
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QY 1 ctgcgtccctcggtgtctgtctgcgacctggccacgcgcttggaatccccaaggactcg 60
DB 5 CTTGCGTTCCCTCGGGGCTTGTCTCGGACCTCGGCGCACCGGCTGGATCCCGCAGAGACTCG 144
QY 61 tgcgtgaagcatggcggtcggtcggtcggtcggtcggtcggtcggtcggtcggtcggtcg 120
DB 145 TGCCTGACAGCATYGGGCGGCGGCGGCGGAGCCGCGGACCCGCGGAGCGACCCGCGCGGGG 204
QY 121 ggcacgcgtgcacacccctctctgtgagagacatccgcgcgcgcgcgcgcgcgcgcgcgcgc 180
DB 205 GGCACCGCTGCGCCACCTTCTGCTGCGAGCATCCGCGCGACACGACCGCGCGGCGACCA 264
QY 181 gtgcgtgcatcagcagcgcgctctcagacatcagcgcgtgtggtggtggtggtggtggtg 240
DB 265 GTGCTGTGATCATGAGCGCGCGCGCTCTACGACATCAGCCGCTGGGCGACAGCGGCGACCG 324
QY 241 gggcagcgcgtctctcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 300
DB 325 GGGGAGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 384
QY 301 ccaatcaagatcgaatttctgtgcaagttctcctcagacccctgttgaattgagaagctgagc 360
DB 385 CCATCAAGATCTCAATTTTGTGGCCAGATCTCTACACGCCCTGTGTGATGTGAGACAGCTGCG 444
QY 361 tccggaagacccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420
DB 445 TCCCGAAGAACCCAGCGAGATGAGCCCTGAAATGCGCACTGGTGTGAGGAGACTTCCGAA 504
QY 421 cctgcaccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
DB 505 CCTGCACACGAGCAGCGAGACATGAAGCTGTTGATGCGCAGTCCACCTTCTTGTGCTTT 564
QY 481 cctactgggcacacatcctgtgcacatgagtgctgagcctgtgcttactactcctcctgag 540
DB 565 CTTACTGGGCGCACATCTGTGGCCAGAGAGTGTGGCTGTGGCTGTCTTATCTTACTCTCTGCG 624
QY 541 tccgtgctgggtggtgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 600
DB 625 TCTGTGGCTGGGTGGCGCAGTGCCTGTGGCGGCTTCTCATCTGACCATCTCTCAGGCTCAGTC 684
QY 601 ctgtgtgtctgcaagcatgacct-gggccatgtcctccatc-ttcaagaagtctctgg-tggaa 657
DB 685 CTGTGTGTCTGACATGACCTGTGGGCGCATGCTTCATCTTTCAGAAAGCTCTGTGTTGAA 744
QY 658 ccaacgttgagcc-----agaagtcgtatgagggcagcgttaagagcttctccgcacac----- 709
DB 745 CCACGTTGGGCCCAAGAAAGCTTCCGTGATGTGGGCGCAGTAAAGGGGCGGTCTTCTCCGGCCCA 804
QY 710 --tggtggaacttcgcgaccttcaggaaccaagcgaagcccaacatcttccacaagaagac 767
DB 805 CTGTGGGAAGAACTTCCGACATCTTCAGACACCGCAAGGCGCAAAATCTCTACAAAGAACG 864
QY 768 cagacgtgac--gtgtggtgcggtcttctcctcctggggg-----agtcagctcgaatgag 821
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DB 865 CAGACGTGACCTGTGGGCGCGGCTTTCCTCTGGGGGAGATCAGACCGAAGGTATG 924
QY 822 gcaagaagaagac---gcagatacctacacacacacacacacacacacacacacacacacacac 875
DB 925 GGCAGAAAAAACCGAGAAATCTTACCTTAAACACAGAAAGACACTTGGACTTCTTCC 984
QY 876 t---gatacgccgcgcgtcgtcacccttgatgaatttgaaatggaatcctgagctaca 932
DB 985 TTGAATGCGCGCGCAGCTTGTACCTCGGGAATTTTGAAGTGGAATACTGGGGTAAAC 1044
QY 933 tgcgtgtg 940
DB 1045 TGGGGGGG 1052
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RESULT 13
BG323412      925 bp      mRNA      linear      EST 27-FEB-2001
LOCUS        602421620F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4559669 5'
DEFINITION   mRNA sequence.
ACCESSION    BG323412
VERSION      BG323412.1 GI:13129849
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
```

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REFERENCE    1 (bases 1 to 925)
AUTHORS      NIH-MGC http://mgc.ncl.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgaabs-remail.nih.gov
              Tissue Procurement: DCDT/DRP
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LILCM1267 row: h column: 06
High quality sequence stop: 711.
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FEATURES
source       1..925
              Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4559669"
/clone_lib="NIH_MGC_14"
/tissue_type="renal cell adenocarcinoma"
/notes="Organ: kidney; Vector: pORF7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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BASE COUNT      181 a      303 c      239 g      202 t
ORIGIN
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Query Match      38.2%; Score 649; DB 10; Length 925;
Best Local Similarity 94.7%; Pred. No. 5.2e-126;
Matches 738; Conservative 0; Mismatches 30; Indels 11; Gaps 6;
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QY 280 cagagatgcttcgtgcttccatcaagatcgaatttggtgcgaagtctcctacag-c 338
DB 2 CACGATGCTTCCGTGCTTCCATCAAGATCTCAATTTGTGGCAAGTCTCAAGTC 61
QY 339 cccgttgattggagagctggtcgcggaagacccagcagatgagccctgaatgcgc 398
DB 62 CCCTGTGATTGGAGAGCTGCTCGGAAGAACCGACGAGATGAGACCCCTGTAATGCCG 121
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.000S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-834-655-1

Query Match 3.3%; Score 55.8; DB 2; Length 1617;
Best Local Similarity 54.7%; Pred. No. 0.00089;
Matches 111; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 1167 acgtgagccctcactttccaccacttggttcagcgagcactcaccatccagatcgagc 1226
DB 1203 ATGTCCACCCGGGTATTGTCACACTGGTTCACGGGTGATGAACTATGATGAGTGCAGC 1262
QY 1227 accactcttcccccagagatgcgagacacactacagccgggtgccccgtgtgcaagt 1286
DB 1263 ACCACTGTTCCCTTCGATGCGCTCCGCCACACTTTTCAAAAGATCCAGCTGCTGTCGAGA 1322
QY 1287 cgctgtgtccagacagcgccctcagctagaaagtgaagcccttcaccacggcgctggtg 1346
DB 1323 CCTGTGCAAAAAGTCAATGTCGATACCAACACCGGTATGATGAGGGAACCTGACG 1382
QY 1347 acatgctcaggtccctgaaag 1369
DB 1383 AGGTCTTAGCCGTCTGAACGAG 1405

RESULT 5
US-08-834-033A-1
Sequence 1, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KNUDZON, DEBORAH
APPLICANT: MURKUT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300, USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-834-033A-1

Query Match 3.3%; Score 55.8; DB 3; Length 1617;
Best Local Similarity 54.7%; Pred. No. 0.00089;
Matches 111; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 1167 acgtgagccctcactttccaccacttggttcagcgagcactcaccatccagatcgagc 1226
DB 1203 ATGTCCACCCGGGTATTGTCACACTGGTTCACGGGTGATGAACTATGATGAGTGCAGC 1262
QY 1227 accactcttcccccagagatgcgagacacactacagccgggtgccccgtgtgcaagt 1286
DB 1263 ACCACTGTTCCCTTCGATGCGCTCCGCCACACTTTTCAAAAGATCCAGCTGCTGTCGAGA 1322
QY 1287 cgctgtgtccagacagcgccctcagctagaaagtgaagcccttcaccacggcgctggtg 1346
DB 1323 CCTGTGCAAAAAGTCAATGTCGATACCAACACCGGTATGATGAGGGAACCTGACG 1382
QY 1347 acatgctcaggtccctgaaag 1369
DB 1383 AGGTCTTAGCCGTCTGAACGAG 1405

RESULT 6
US-09-363-574-1
Sequence 1, Application US/09363574
Patent No. 6136574
GENERAL INFORMATION:
APPLICANT: KNUDZON, DEBORAH
APPLICANT: MURKUT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:

APPLICATION NUMBER: US/08/852,401
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa L.
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: FER2159PO030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4776 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-852-401-1

Query Match 2.6%; Score 44.2; DB 2; Length 4776;
Best Local Similarity 48.2%; Pred. No. 0.45;
Matches 124; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 697 ctctccgcccactggtggaacttcgcgcaactccagaccagccaagccaacatcct 756
DB 2389 CTTCTGTCGCCGCCGAGACGCCGACCTGACATG6GCGCAACCCGACATCCGCGAGT 2448
QY 757 ccaaaagagaccagactgagtcggtgagccgctctctcgtggggagatcgcgtga 816
DB 2449 CGCCAAAGTCTGAGTTGCGTGACCGGGGGTGGACGGCTTCCGGATCGACGTCGC 2508
QY 817 gtatggaagaagaagacgacatccactcaacacgaagacactgtactctcct 876
DB 2509 CCACGGCATGATCAAGACACCCGACGCTGCCGACACCGGGCTGACACGACATCTCC 2568
QY 877 gatcgcccgccgctgtcacacctgtgtaacttgaagtgaatcgtacatgct 936
DB 2569 GCTCGGCGGGGCCGCTGCTCTTCTGACACAGACAGAGTGACGCGCATCTACCGGA 2628
QY 937 ggtgcatgagtggtg 953
DB 2629 GTGGCGGAGCTGCTGG 2645

RESULT 15
US-09-411-687A-29
Sequence 29, Application US/09411687A
Patent No. 6287813
GENERAL INFORMATION:
APPLICANT: Fusseneegger, Martin
APPLICANT: Thompson, Charles J.
APPLICANT: Bailey, James E.
TITLE OF INVENTION: ANTIBIOTIC-BASED GENE REGULATION SYSTEM
FILE REFERENCE: 9931-0005-999
CURRENT APPLICATION NUMBER: US/09/411,687A
CURRENT FILING DATE: 1999-10-04
PRIOR APPLICATION NUMBER: US 09/298,768
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 780
TYPE: DNA
ORGANISM: Streptomyces coelicolor
US-09-411-687A-29

Query Match 2.6%; Score 43.8; DB 4; Length 780;
Best Local Similarity 45.9%; Pred. No. 0.35;
Matches 150; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 145 ggaagacatccgcgcgcagaccagcccgagacaaagtgtgtatcatgagcgcggt 204

DB 372 ggtgcgcaacccctgtctgctccggtctgtcgcaactcaacatcgcgcgcacatc 431
QY 205 ctacgacatcagccgctgtggcagcagccacccaggggagccgctcctcatcgccacca 264
DB 432 gctgctcttcctccgcgcggtgacgaacgctgtgcgcgcagcggtccgcgcgcacg 491
QY 265 cggcgtgaggaagcgcaggaatgcttcgcttcctcatcaaatctcaatttltgctg 324
DB 492 cctgaacggcgccatctcgccgcttccagtctgctacggtacggcaccatcgaggg 551
QY 325 caagtctctaacagccctgtgtatggaagctgtgtccggaagaacccacagagatgg 384
DB 552 ccgcttctccgcgcggtgtgcggaacccggtgtgagtcggagagatcttccaggaatc 611
QY 385 acccctgaatgcgaagctgtgtcgaagcttcgagccctgcagccagcgagcgagacat 444
DB 612 gatgaacgcggtgacaggaagtgtccggaacacgcggtgtcatcgagagcgagacat 671
QY 445 gaagctgtttgaltgccagtlccacatc 471
DB 672 catggcgccgcggggtgcggaacacgt 698

Search completed: October 8, 2002, 03:43:29
Job time: 12304 sec

Tue Oct 8 10:29:13 2002

us-09-806-088-2.rni

Page 9

